

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 11:04:56 ; Search time 237 Seconds
(without alignments)
35.723 Million cell updates/sec

Title: US-10-657-851-37
Perfect score: 62
Sequence: 1 RLCRIVVIRVCR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	155	1	BCTN1_BOVIN
2	52	83.9	155	1	BCTN1_SHEEP
3	42	67.7	662	2	Q9C5J0_ARATH
4	42	67.7	662	2	Q22173_ARATH
5	42	67.7	2660	2	Q7QL19_ANOGA
6	40	64.5	569	2	Q528U7_ORYZA
7	40	64.5	605	2	Q41464_GIBZE
8	40	64.5	1514	2	Q4UAU0_THEAN
9	39	62.9	142	2	Q8KCL5_HUMAN
10	39	62.9	359	2	Q8L544_ORYZA
11	39	62.9	630	2	Q74AJ6_GOSL
12	39	62.9	695	2	Q4P363_USTMA
13	39	62.9	820	2	Q9FFK8_ARATH
14	39	62.9	997	2	Q41711_GIBZE
15	38.5	62.1	145	2	Q8G532_BIFLO
16	38	61.3	147	2	Q6CM89_KUOLA
17	38	61.3	203	2	Q89CN2_BRAJA
18	38	61.3	342	2	Q4SZL3_TETNG
19	38	61.3	343	2	Q22043_ARATH
20	38	61.3	343	2	Q4NE13_9MICC
21	38	61.3	433	2	Q5YWC4_NOCFA
22	38	61.3	497	2	Q862R6_9TRYP
23	38	61.3	610	2	Q9NA53_CAEEL
24	38	61.3	681	2	Q9U1S8_CAEEL
25	38	61.3	1381	2	Q4QDQ6_LEIMA
26	38	61.3	1827	2	Q4Q123_LEIMA
27	38	61.3	2148	2	Q18183_CAEEL
28	37	59.7	82	2	Q6CY53_BIFLO
29	37	59.7	108	2	Q6N7R8_RHOPA
30	37	59.7	160	2	Q59X76_CANAL
31	37	59.7	160	2	Q59XC4_CANAL

32	37	59.7	176	2	Q7RS70_PLAYO	Q7RS70 plasmodium
33	37	59.7	200	2	Q8SRF8_ENCCU	Q8SRF8 encephalito
34	37	59.7	208	2	Q81428_PLAY7	Q81428 plasmodium
35	37	59.7	279	2	Q4LG14_BURK	Q4LG14 burkholderi
36	37	59.7	309	2	Q7RQC6_PLAYO	Q7RQC6 plasmodium
37	37	59.7	347	2	Q7RBI8_PLAYO	Q7RBI8 plasmodium
38	37	59.7	382	2	Q89DY2_BRAJA	Q89DY2 bradyrhizob
39	37	59.7	395	2	Q960D9_DROME	Q960D9 drosophila
40	37	59.7	395	2	Q9VM45_DROME	Q9VM45 drosophila
41	37	59.7	553	2	Q6DK23_TOXGO	Q6DK23 toxoplasma
42	37	59.7	727	2	Q5G466_LYCES	Q5G466 lycopersico
43	37	59.7	833	2	Q653R0_ORYZA	Q653R0 oryza sativ
44	37	59.7	934	2	Q4FYM1_LEIMA	Q4FYM1 leishmania
45	36.5	58.9	320	2	Q5B248_EMENI	Q5B248 aspergillus
46	36	58.1	71	2	Q4XNL1_PLACH	Q4XNL1 plasmodium
47	36	58.1	80	2	Q4Z0A0_PLABE	Q4Z0A0 plasmodium
48	36	58.1	165	2	Q49758_MYCLE	Q49758 mycobacteri
49	36	58.1	166	2	Q4SWC0_TETNG	Q4SWC0 tetraodon n
50	36	58.1	181	2	Q5UN24_MIMIV	Q5UN24 mimivirus.
51	36	58.1	219	2	Q9A9J3_CAUCR	Q9A9J3 caulobacter
52	36	58.1	276	2	Q9QJ35_9BETA	Q9QJ35 human herpe
53	36	58.1	276	2	Q9WT30_9BETA	Q9WT30 human herpe
54	36	58.1	316	2	Q7RSR4_GIALA	Q7RSR4 giardia lam
55	36	58.1	328	2	Q5L9S8_BACFN	Q5L9S8 bacteroides
56	36	58.1	344	2	Q9XU00_CAEEL	Q9XU00 caenorhabdi
57	36	58.1	364	2	Q8L535_ORYZA	Q8L535 oryza sativ
58	36	58.1	379	2	Q8T206_DICDI	Q8T206 dictyosteli
59	36	58.1	391	1	EPT1_YEAST	P22140 saccharomyc
60	36	58.1	446	2	Q9V5B0_DROME	Q9V5B0 drosophila
61	36	58.1	708	2	Q7F803_ORYZA	Q7F803 oryza sativ
62	36	58.1	815	2	Q805B9_BRARE	Q805B9 brachydanio
63	36	58.1	815	2	Q8AYP3_BRARE	Q8AYP3 brachydanio
64	36	58.1	817	2	Q8JG38_BRARE	Q8JG38 brachydanio
65	36	58.1	853	2	Q8Q504_9RETR	Q8Q504 feline immu
66	36	58.1	856	2	Q6FXG3_CANGA	Q6FXG3 candida gla
67	36	58.1	909	2	Q5ZEL8_ORYZA	Q5ZEL8 oryza sativ
68	36	58.1	1284	2	Q7PVF3_ANOGA	Q7PVF3 anopheles g
69	36	58.1	1357	2	Q59DX2_DROME	Q59DX2 drosophila
70	35.5	57.3	472	2	Q4YRN6_PLABE	Q4YRN6 plasmodium
71	35.5	57.3	2761	2	Q19522_CAEEL	Q19522 caenorhabdi
72	35.5	57.3	3008	2	Q60MN8_CAEBR	Q60MN8 caenorhabdi
73	35	56.5	38	2	Q731N5_BACC1	Q731N5 bacillus ce
74	35	56.5	131	2	Q6IM51_DROME	Q6IM51 drosophila
75	35	56.5	134	2	Q9EX49_STRCO	Q9EX49 streptomyce
76	35	56.5	214	2	Q64S75_BACPR	Q64S75 bacteroides
77	35	56.5	225	2	Q4LIU4_BURK	Q4LIU4 burkholderi
78	35	56.5	233	2	Q8DWC3_STRMU	Q8DWC3 streptococc
79	35	56.5	234	2	Q5T7M2_HUMAN	Q5T7M2 homo sapien
80	35	56.5	241	1	TNR18_HUMAN	Q9Y5U5 homo sapien
81	35	56.5	241	2	Q5U014_HUMAN	Q5U014 homo sapien
82	35	56.5	255	1	NFI_AERPE	Q9Y5E5 aeropyrum p
83	35	56.5	255	2	Q5T7K5_HUMAN	Q5T7K5 homo sapien
84	35	56.5	271	2	Q5SNS9_BRARE	Q5SNS9 brachydanio
85	35	56.5	304	2	Q5TTS3_ANOGA	Q5TTS3 anopheles g
86	35	56.5	320	2	Q6MPU8_BDEBA	Q6MPU8 bdellovibri
87	35	56.5	368	2	Q8A835_BACTN	Q8A835 bacteroides
88	35	56.5	414	2	Q8YRFE_ANASP	Q8YRFE anabaena sp
89	35	56.5	441	2	Q4S8L3_TETNG	Q4S8L3 tetraodon n
90	35	56.5	466	2	Q7XQNO_ORYZA	Q7XQNO oryza sativ
91	35	56.5	470	2	Q4UFC4_THEAN	Q4UFC4 theileria a
92	35	56.5	477	2	Q9BU21_HUMAN	Q9BU21 homo sapien
93	35	56.5	505	2	Q9JTF0_NEIMA	Q9JTF0 neisseria m
94	35	56.5	507	2	Q6Z4L0_ORYZA	Q6Z4L0 oryza sativ
95	35	56.5	520	2	Q5T5R6_HUMAN	Q5T5R6 homo sapien
96	35	56.5	556	2	Q4SYE4_TETNG	Q4SYE4 tetraodon n
97	35	56.5	573	2	Q4K623_PSEF5	Q4K623 pseudomonas
98	35	56.5	593	2	Q8BHX6_MOUSE	Q8BHX6 mus musculu
99	35	56.5	598	2	Q4RUY6_TETNG	Q4RUY6 tetraodon n
100	35	56.5	687	2	Q4SM47_TETNG	Q4SM47 tetraodon n

ALIGNMENTS

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RESULT 1
BCTN1_BOVIN STANDARD; PRT; 155 AA.
AC P22226;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cyclic dodecapeptide precursor (Bactenecin 1) (Bac1).
GN Name=BAC1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=33093170; PubMed=1459251; DOI=10.1016/0014-5793(92)80971-I;
RA Storicci P., del Sal G., Schneider C., Zanetti M.;
RT "cDNA sequence analysis of an antibiotic dodecapeptide from
neutrophils.";
RL FEBS Lett. 314:187-190(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Scocchi M., Wang S., Zanetti M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PROTEIN SEQUENCE OF 144-155.
RC TISSUE=Neutrophil;
RX MEDLINE=88257074; PubMed=3290210;
RA Romeo D., Skerlavaj B., Bolognesi M., Gennaro R.;
RT "Structure and bactericidal activity of an antibiotic dodecapeptide
purified from bovine neutrophils.";
RL J. Biol. Chem. 263:9573-9575(1988).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=96300243; PubMed=8706679;
RA Storicci P., Tossi A., Lenarcic B., Romeo D.;
RT "Purification and structural characterization of bovine cathelicidins,
precursors of antimicrobial peptides.";
RL Eur. J. Biochem. 238:769-776(1996).
CC -1- FUNCTION: Potent microbicidal activity, active against
Staphylococcus aureus and Escherichia coli.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Large granules of neutrophils.
CC -1- SIMILARITY: Belongs to the cathelicidin family.
CC
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the European Bioinformatics Institute. There are no restrictions on its
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removed.
CC
CC EMBL; L08834; AAA50615.1; -; mRNA.
CC EMBL; Y09472; CAA70617.1; -; Genomic DNA.
CC PIR; S27018; S27018.
CC HSSP; P32196; 1KWI.
CC SMR; P22226; 30-130.
CC InterPro; IPR001894; Cathelicidin.
CC PANTHER; PTHR10206; Cathelicidin; 1.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidin; 1.
CC PROSITE; PS00946; CATHELICIDINS_1; 1.
CC PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 143 Cyclic dodecapeptide.
FT PEPTIDE 144 155 Pyrrolidone carboxylic acid.
FT MOD_RES 30 30 By similarity.
FT DISULFID 85 96

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FT DISULFID 107 124 By similarity.
FT DISULFID 146 154
FT VARIANT 128 155 Q -> R.
SQ SEQUENCE 155 AA; 17600 MW; 008CD7DC6CB91BF9 CRC64;

Query Match 100.0%; Score 62; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.003; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 RLCRIWVIRVCR 12
|||||
Db 144 RLCRIWVIRVCR 155

RESULT 2
BCTN1_SHEEP STANDARD; PRT; 155 AA.
AC P54230;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cyclic dodecapeptide precursor (Bactenecin 1) (Bac1).
GN Name=BAC1A; Synonyms=DODEA;
GN and
GN Name=BAC1B; Synonyms=DODEB;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3;
RA Bagella L., Scocchi M., Zanetti M.;
RT "cDNA sequences of three sheep myeloid cathelicidins.";
RL FEBS Lett. 376:225-228(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Liver;
RX MEDLINE=98121317; PubMed=9461419; DOI=10.1016/S0378-1119(97)00569-6;
RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT "Localization and genomic organization of sheep antimicrobial peptides
genes.";
RL Gene 206:85-91(1998).
CC -1- FUNCTION: Potent microbicidal activity, active against
Staphylococcus aureus and Escherichia coli (By similarity).
CC -1- SIMILARITY: Belongs to the cathelicidin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; L46853; AAA85469.1; -; mRNA.
CC EMBL; U60595; AAB49710.1; -; Genomic DNA.
CC EMBL; U60596; AAB49711.1; -; Genomic DNA.
CC PIR; S68229; S68229.
CC HSSP; P32196; 1KWI.
CC SMR; P54230; 30-130.
CC InterPro; IPR001894; Cathelicidin.
CC PANTHER; PTHR10206; Cathelicidin; 1.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidin; 1.
CC PROSITE; PS00946; CATHELICIDINS_1; 1.
CC PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 143 By similarity.
FT PEPTIDE 144 155 Cyclic dodecapeptide.
FT MOD_RES 30 30 Pyrrolidone carboxylic acid (By
similarity).
FT

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OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702,
RN [1]
RP
RA NUCLEOTIDE SEQUENCE.
RZ Rounleay S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
SA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP
RA NUCLEOTIDE SEQUENCE.
RZ Town C.D., Kaul S.;
SA Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP
RA NUCLEOTIDE SEQUENCE.
RZ Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
SA Goldemith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carlinici P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Eckert J.R.,
RA Theologis A.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP
RA NUCLEOTIDE SEQUENCE.
RZ Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,
SA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
RA Southwick A., Davila R.W., Eckert J.R., Theologis A.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC00391; AA87097.1; - ; Genomic DNA.
DR DR EMBL; AY050859; AAA92796.1; - ; mRNA.
DR ENBL; AV079389; AAL85120.1; - ; mRNA.
DR FIR; TO0497; TO0497.
DR HSSP; P11940; IGVJ.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR DR GO; GO:0003723; rRNA binding; IEA.
DR GO; GO:000398; P:nuclear RNA splicing, via spliceosome; IEA.
DR InterPro; IPRO12677; a_b_plait_nuc_bd.
DR InterPro; IPRO06515; PABP_1234.
DR InterPro; IPRO02004; PABP_HYD.
DR InterPro; IPRO00504; RNPI_RNA_bd.
DR Pfam; PF00658; PABP; 1.
DR Pfam; PF00076; RM; 1; 4.
DR SMART; SM00517; PolyA; 1.
DR SMART; SM00360; RRM; 4.
DR TIGRFAMs; TIGR01628; PABP-1234; 1.
DR PROSITE; PS0102; RRM; 4.
SQ SEQUENCE 662 AA; 71653 MW; 448481E183DF339E CRC64;

Query Match 67.7%; Score 42; DB 2; Length 662;
Best Local Similarity 54.5%; Pred. No. 49;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCRIIVRVRCR 12
Db 69 VCQVDSVRVC 79

RESULT 5
Q7QL19 ANOGA
ID Q7QL19_ANOGA PRELIMINARY; PRT; 2660 AA.
AC Q7QL19;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000014551 (Fragment).
GN ORFNames=ENSANGG00000012062;
GS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
QC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Culicidae;

DR EMBL; AACM01000323; EAA72955.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 605 AA; 66248 MW; A7E3E637F1A839BB CRC64;

Query Match 64.5%; Score 40; DB 2; Length 605;
 Best Local Similarity 63.6%; Pred. No. 1e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 LCRIVWIRVC 12
 Db 502 IMRILVLRVC 512
 : |||: |||
 : |||: |||

RESULT 8

Q4UAU0 THEAN PRELIMINARY; PRT; 1514 AA.

ID Q4UAU0;
 AC Q4UAU0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=TA17370;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
 OC Theileria.
 OX NCBI_TaxID=5874;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Ankara isolate clone C9;
 RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
 RA Hall N., Barrell B.G.;
 RT "The chromosome 3 genome sequence of Theileria annulata."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR940352; CA176061.1; -; Genomic_DNA.
 KW Hypothetical protein.

SQ SEQUENCE 1514 AA; 174664 MW; 8CB30650A083CASA CRC64;

Query Match 64.5%; Score 40; DB 2; Length 1514;
 Best Local Similarity 45.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 2 LCRIVWIRVC 12
 Db 1372 LCKVIVTKCR 1382
 : |||: |||
 : |||: |||

RESULT 9

O6KC15 HUMAN PRELIMINARY; PRT; 142 AA.

ID O6KC15;
 AC O6KC15;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hepcidin antimicrobial peptide (fragment).

GN Name=HAMP;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

OX NCBI_TaxID=9606;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Zaahl M.G., Merryweather-Clarke A.T., Kotze M.J., van der Merwe S.,
 RA Warnich L., Robson K.J.H.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ715525; CAG29368.1; -; Genomic_DNA.
 FT NON TER 142 142

SQ SEQUENCE 142 AA; 14932 MW; 3A17FB244F2D8768 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 142;
 Best Local Similarity 60.0%; Pred. No. 41;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 LCRIVWIRVC 11
 Db 92 LCRVSVLRAC 101
 : |||: |||
 : |||: |||

RESULT 10

Q8LS44 ORYSA PRELIMINARY; PRT; 359 AA.

ID Q8LS44;
 AC Q8LS44;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein OSJNB0072F04.12 (Hypothetical protein OSJNB0072F04.6).
 GN Name=OSJNB0072F04.6; ORFNames=OSJNB0072F04.12;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Wang R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
 RA Sasaki C., Henry D., Oates R., Simmons J.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RA Wang R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R.,
 RA Rambo T., Sasaki C., Henry D., Oates R., Simmons J.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.

RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 chromosome 10."
 RL Science 300:1566-1569(2003).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.

RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC092553; AAM23246.1; -; Genomic_DNA.
 DR EMBL; AC122147; AAM47617.1; -; Genomic_DNA.

DR EMBL; AE017053; AAP51984.1; -; Genomic_DNA.
 DR Gramene; Q8LS44; -;

DR GO; GO:0006512; P:ubiquitin cycle; IEA.

DR InterPro; IPR001810; F-box.

DR Pfam; PF00646; F-box; 1.

DR Hypothetical protein.

SQ SEQUENCE 359 AA; 40204 MW; 208B10C4437447C6 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 359;
 Best Local Similarity 63.6%; Pred. No. 97;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LCRIVWIRVC 11
 Db 154 LCRVLRVVC 164
 : |||: |||
 : |||: |||

RESULT 11

Q74AJ6 GEOSL PRELIMINARY; PRT; 630 AA.

ID Q74AJ6;
 AC Q74AJ6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Isoamylase family protein.
 GN OrderedLocusNames=GSU2358;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;

RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methé B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Uitterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments";
RT Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR35732.1; -; Genomic_DNA.
DR TIGR; GS02358;
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR004193; Glyco_hydro_13n.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF02922; Isoamylase N; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 630 AA; 70095 MW; CE8192F12D3F66EA CRC64;

Query Match 62.9%; Score 39; DB 2; Length 630;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RIVIVR 12
Db 535 RVVVR 543

RESULT 12
Q4P363 USTWA
ID Q4P363 USTWA PRELIMINARY; PRT; 695 AA.
AC Q4P363;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=UM05450.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OC NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachi H., Armbruster J., Bachanteang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhaltier B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Callymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kanvaseelis M., Karlsson E.,
RA Kells C., Kieu A., Kibner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokvitsang T., Lokvitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,

RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Teamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL; AACP01000195; EAK86345.1; -; Genomic_DNA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Hypothetical protein.
SQ SEQUENCE 695 AA; 76808 MW; 3C69674A1A475CD8 CRC64;

Query Match 62.9%; Score 39; DB 2; Length 695;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLCEIVVIR 9
Db 305 RLCEIVVIR 313

RESULT 13
Q9PFK8 ARATH
ID Q9PFK8 ARATH PRELIMINARY; PRT; 820 AA.
AC Q9PFK8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similarity to unknown protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT clones";
RT DNA Res. 4:215-230(1997).
RL EMBL; AB005237; BAB09660.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003482; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:protein ubiquitination; IEA.
DR GO; GO:0016567; P:regulation of transcription; IEA.
DR InterPro; IPR006058; 2Pe2s fd BS.
DR InterPro; IPR000967; Znf_NFX1.

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DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF01422; zf-NF-X1_6.
DR SMART; SM00184; RING; 1.
DR SMART; SM00438; Znf_NFX; 7.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN 2.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN 1.
SQ SEQUENCE 820 AA; 92073 MW; CB8CF9D64D18D30F CRC64;

Query Match 62.9%; Score 39; DB 2; Length 820;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
Db 375 CRIVVTKSR 384
|||||:||||

RESULT 14
Q41711 GIBZE
ID Q41711 GIBZE PRELIMINARY; PRT; 997 AA.
AC Q41711; 2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORENAMES=FG06997.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Arrhen B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeAtellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal A., Karatas A.,
RA Kalls C., Landers T., Levine R., Lindblad-Toh K., Liu J., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor T., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACW0100289; EAA76192.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 997 AA; 107426 MW; 59B2130524C4E72D CRC64;

Query Match 62.9%; Score 39; DB 2; Length 997;
Best Local Similarity 63.6%; Pred. No. 2.5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLRCRIVRVC 11
Db 93 RLRSRVRLC 103
|||||:|||||

RESULT 15
Q8G532 BIFLO
ID Q8G532 BIFLO PRELIMINARY; PRT; 145 AA.
AC Q8G532;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=BL1188;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 2705;
RA Schell M.A., Kamirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014295; AAN24993.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 145 AA; 16921 MW; C17084D9BE1608C8 CRC64;

Query Match 62.1%; Score 38.5; DB 2; Length 145;
Best Local Similarity 61.5%; Pred. No. 51;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 RLRCRIVRVC 12
Db 28 RLRCRIVRVC 40
|||||:|||||

RESULT 16
Q6CM89 KLUJA
ID Q6CM89 KLUJA PRELIMINARY; PRT; 147 AA.
AC Q6CM89;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarity.
GN OrderedLocuNames=KLA0E22165g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RL PubMed=15229592; DOI=10.1038/nature02579;
RX Dujon B., Sherman D., Fischer G., Durrans P., Casaregola S.,
RX Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RX Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RX Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RX Boissone A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RX Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RX Hantraye P., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RX Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RX Nicaud J.-M., Nikolski M., Oztas S., Oxier-Kalogeropoulos O.,
RX Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RX Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RX Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RX Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RX Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382125; CAH00037.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 147 AA; 16993 MW; DAD35A01EDC67791 CRC64;

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Query Match 61.3%; Score 38; DB 2; Length 147;
 Best Local Similarity 50.0%; Pred. No. 64;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLCRIVVIRV 10
 DB 124 RMCRIYVRI 133
 |||:|:|

RESULT 17

Q89CN2 BRAJA
 ID Q89CN2 BRAJA PRELIMINARY; PRT; 203 AA.
 AC Q89CN2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE B117765 protein.
 GN OrderedLocusNames=b117765;
 OS Bradyrhizobium japonicum.
 OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriiguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shingo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; BA000040; BAC53030.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 203 AA; 23052 MW; 6E92DA8F851103C7 CRC64;

Query Match 61.3%; Score 38; DB 2; Length 203;
 Best Local Similarity 50.0%; Pred. No. 86;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLCRIVVIRV 10
 DB 11 RLCRLAILRI 20
 |||:|:|

RESULT 18

Q4SZL3 TETNG
 ID Q4SZL3 TETNG PRELIMINARY; PRT; 342 AA.
 AC Q4SZL3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 14 SCAP11586, whole genome shotgun sequence.
 GN ORFNames=GSTENG0009791001;
 OS Tetraodon nigroviridis (Green puffer).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAE01011586; CAF93919.1; -; Genomic DNA.
 SQ SEQUENCE 342 AA; 37353 MW; 5F9CFC8BC4D954DD CRC64;

Query Match 61.3%; Score 38; DB 2; Length 342;
 Best Local Similarity 54.5%; Pred. No. 1.4e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVC 11
 DB 89 RGCRRVLRSC 99
 |||:|:|

RESULT 19

O22043 ARATH
 ID O22043 ARATH PRELIMINARY; PRT; 343 AA.
 AC O22043;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Geranyl geranyl pyrophosphate synthase.
 GN Names=GGPS6;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98009970; PubMed=9349257; DOI=10.1023/A:1005898805326;
 RA Zhu X., Suzuki K., Saito T., Okada K., Tanaka K., Nakagawa T.,
 RA Matsuda H., Kawamukai M.;
 RT "Geranylgeranyl pyrophosphate synthase encoded by the newly isolated
 gene GGPS6 from Arabidopsis thaliana is localized in mitochondria.";
 RL Plant Mol. Biol. 35:331-341(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20223719; PubMed=10759500; DOI=10.1104/pp.122.4.1045;
 RA Okada K., Saito T., Nakagawa T., Kawamukai M., Kamiya Y.;
 RT "Five geranylgeranyl diphosphate synthases expressed in different
 RT organs are localized into three subcellular compartments in
 RT Arabidopsis.";
 RL Plant Physiol. 122:1045-1056(2000).
 DR EMBL; AB000835; BAA23157.1; -; Genomic DNA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
 DR InterPro; IPR000092; Polyprenyl synt.
 DR Pfam; PF00348; polyprenyl synt; 1.
 DR PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
 DR PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
 SQ SEQUENCE 343 AA; 37509 MW; 88E84328A1802A7F CRC64;

Query Match 61.3%; Score 38; DB 2; Length 343;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVIVRVC 11
 DB 2 LCKIIIMRPC 11
 |||:|:|

RESULT 20


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DR EMBL; AL132862; CAB60545.2; -; Genomic_DNA.
DR Ensemble; Y73F8A.19; Caenorhabditis elegans.
DR WormBase; WBGene00006441; Y73F8A.19.
DR WormPep; Y73F8A.19; CE322997.
DR InterPro; IPR010734; Copine.
DR Pfam; PF07002; Copine; 1
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 610 AA; 6913 MW; F79787143086FC74 CRC64;

Query Match 61.3%; Score 38; DB 2; Length 610;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
Db 285 RLCRYQQLRVC 295
|||||:||||

RESULT 24
Q9U1S8 CAEEL
ID Q9U1S8 CAEEL PRELIMINARY; PRT; 681 AA.
AC Q9U1S8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Y6D1A.1.
GN ORFNames=Y6D1A.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL032651; CAB60580.1; -; Genomic_DNA.
DR Ensemble; Y6D1A.1; Caenorhabditis elegans.
DR WormBase; WBGene00012195; Y6D1A.1.
DR WormPep; Y6D1A.1; CE21324.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 681 AA; 79729 MW; D78FA2A846D9A4BF CRC64;

Query Match 61.3%; Score 38; DB 2; Length 681;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 12
Db 639 CRLVKLHVCR 648
|||||:||||

RESULT 25
Q4QDG6 LEIMA
ID Q4QDG6 LEIMA PRELIMINARY; PRT; 1381 AA.
AC Q4QDG6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF19.0560;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S.; Murphy L.; Ivens A.C.; Berriman M.; Blackwell J.;
SA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
SA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,
SA

RA Bianchetti G., Borzym K., Bothe G., Bruschi C., Ciarloni L.,
RA Duesterhoeft A., Fuchs M., Gabel C., Goffeau A., Hilbert H.,
RA Klages S., Kube M., Marra M., Masuy D., Mueller-Auer S., Pohl T.,
RA Purnelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
RA Tosato V., Volckaert G., Wambutt R., Wedler H., Zimmermann M.,
RA Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CRO05258; CAJ07140.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1381 AA; 145460 MW; 11E833812BB4083D CRC64;

Query Match 61.3%; Score 38; DB 2; Length 1381;
Best Local Similarity 55.8%; Pred. No. 5.2e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
Db 965 CRLMWLRIC 973
|||||:||||

RESULT 26
Q4Q1Z3 LEIMA
ID Q4Q1Z3 LEIMA PRELIMINARY; PRT; 1827 AA.
AC Q4Q1Z3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF36.0830;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S.; Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CTO05272; CAJ09036.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1827 AA; 197974 MW; B6CE402CC02AA056 CRC64;

Query Match 61.3%; Score 38; DB 2; Length 1827;
Best Local Similarity 54.5%; Pred. No. 6.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
Db 291 RNCRVAVTVC 301
|||||:||||

RESULT 27
Q18183 CAEEL
ID Q18183 CAEEL PRELIMINARY; PRT; 2148 AA.
AC Q18183;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=C25H3.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).

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DR EMBL; U29535; AAK31453.2; -; Genomic DNA.
DR Ensembl; C25H3.8; Caenorhabditis elegans.
DR WormBase; WBGene00016117; C25H3.8.
DR WormPeP; C25H3.8; CE32142.
DR GO; GO:0008104; P:protein localization; IEA.
DR InterPro; IPR002202; HMG-CoA_red.
DR InterPro; IPR000772; Ricin B_lectin.
DR InterPro; IPR009543; VPSAP.
DR Pfam; PF06650; DUF1162; 1.
DR PROSITE; PS00318; HMG COA REDUCTASE_2; UNKNOWN_1.
DR PROSITE; PS50231; RICIN B_LECTIN; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 2148 AA; 243201 MW; B61FDE04C39768BA CRC64;

Query Match 61.3%; Score 38; DB 2; Length 2148;
Best Local Similarity 54.5%; Pred. No. 7.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 12
Db 2012 LCRVIRPCLR 2022

RESULT 28
Q8CY53 BIFLO PRELIMINARY; PRT; 82 AA.
AC Q8CY53_
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated stage III sporulation protein J (SpoIIJ) homolog.
GN OrderedLocusNames=BL0776;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwielen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the OXAL/oxaA family.
DR EMBL; AE014295; AAN24591.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0051205; P:protein insertion into membrane; IEA.
DR InterPro; IPR001708; Innermemb_insert.
DR Pfam; PF02096; 60KD_IMP; 1.
DR Complete proteome; Transmembrane.
SQ SEQUENCE 82 AA; 9631 MW; 4563B42B4ACF94C4 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 82;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 11
Db 10 MCLVLIIRIC 19

RESULT 29
Q6N7R8 RHOPA PRELIMINARY; PRT; 108 AA.
AC Q6N7R8_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein precursor.

OrderedLocusNames=RPA2188;
Rhodopseudomonas palustris.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=1076;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572600; CA827629.1; -; Genomic DNA.
DR Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 42 Potential.
SQ SEQUENCE 108 AA; 11577 MW; DB263C3BD4E160F0 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 108;
Best Local Similarity 58.3%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 12
Db 49 RACRPDVMRLCR 60

RESULT 30
Q59X76 CANAL PRELIMINARY; PRT; 160 AA.
AC Q59X76_
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CA019.8234;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Duncan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AACQ01000109; EAK95105.1; -; Genomic DNA.
DR Hypothetical protein.
SQ SEQUENCE 160 AA; 19544 MW; 7B94842C749E2153 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 160;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
Db 11

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Db          22 RLCFVWEYRVC 32

RESULT 31
ID Q59XC4 CANAL PRELIMINARY; PRT; 160 AA.
AC Q59XC4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE DE Hypothetical protein.
GN ORFNames=CaO19.601;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACQ01000108; EAK95151.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 160 AA; 19574 MW; 7B948430049E2153 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 160;
Best Local Similarity 63.6%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVC 11
   |||:|:|
Db          22 RLCFVWEYRVC 32

RESULT 32
ID Q7RS70 PLAYO PRELIMINARY; PRT; 176 AA.
AC Q7RS70;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Putative yir1 protein (Fragment).
GN Names=PY00495;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooli T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Xoo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaiibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

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RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000136; EAA16350.1; -; Genomic_DNA.
DR InterPro; IPR006477; Yir_bir_cir.
DR Pfam; PF06022; Cir_Bir_Yir; 1.
DR TIGRFAMs; TIGR01590; Yir-bir-cir_Pla; 1.
FT NON_TER 176
SQ SEQUENCE 176 AA; 20430 MW; 4DD3C720C2B537B0 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 176;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RLCRIVVIRVC 11
   |||:|:|
Db          9 LCKIVSIHIC 18

RESULT 33
ID Q8SRF8 ENCCU PRELIMINARY; PRT; 200 AA.
AC Q8SRF8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE CALCINEURIN BETA SUBUNIT
DE OrderedLocusNames=SCU08.0160;
GN Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590448; CAD26322.1; -; Genomic_DNA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR011992; EF-Hand_type.
DR Pfam; PF00036; ehand; 2.
DR SMART; SM00054; EFh; 2.
KW Complete proteome; Repeat.
SQ SEQUENCE 200 AA; 23929 MW; 3F0A4E2910B87701 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 200;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVC 10
   |||:|:|
Db          115 RLCRNVLIRI 124

RESULT 34
ID Q8I428 PLAF7 PRELIMINARY; PRT; 208 AA.
AC Q8I428;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein PFE0365c.

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GN Name=PFE0365c;
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=3D7;
 RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
 RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
 RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
 RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
 RL Nature 419:527-531(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=3D7;
 RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
 RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
 .RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL929351; CAD51439.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 208 AA; 24045 MW; C319C77E9B6C898E CRC64;
 Query Match 59.7%; Score 37; DB 2; Length 208;
 Best Local Similarity 40.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LCRIVIRVC 11
 Db 158 ICLVIRVC 167

RESULT 35
 Q4LG14_9BURK PRELIMINARY; PRT; 279 AA.
 AC Q4LG14;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Helix-turn-helix, AraC type.
 OS ORFNames=Scen2424DRAFT_7061;
 OS Burkholderia cenocepacia HI2424.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
 OX NCBI_TaxID=331272;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HI2424;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
 RA Hammon N., Israni S., Pittluck S., Richardson P.;
 RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia HI2424.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HI2424;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Burkholderia cenocepacia HI2424.";

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAL01000179; EAM15176.1; -; Genomic_DNA.
 SQ SEQUENCE 279 AA; 30440 MW; 0E5B622E5CAC01D8 CRC64;
 Query Match 59.7%; Score 37; DB 2; Length 279;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LCRIVIRVC 12
 Db 141 RLCEVLMIRLR 152

RESULT 36
 Q7RQC6_PLAYO PRELIMINARY; PRT; 309 AA.
 ID Q7RQC6_PLAYO PRELIMINARY;
 AC Q7RQC6;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative yirI protein.
 GN Name=PY01174;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAL01000309; EAA20464.1; -; Genomic_DNA.
 DR InterPro; IPR006477; Yir_Bir_cir.
 DR Pfam; PF06022; Cir_Bir_Yir; I.
 DR TIGRFAMs; TIGR01590; Yir-bir-cir_Pla; 1.
 SQ SEQUENCE 309 AA; 35666 MW; 8E974ACA323D8BFF CRC64;
 Query Match 59.7%; Score 37; DB 2; Length 309;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 LCRIVIRVC 11
 Db 9 LCKIVSIHIC 18

RESULT 37
 Q7RB18_PLAYO PRELIMINARY; PRT; 347 AA.
 ID Q7RB18_PLAYO PRELIMINARY;
 AC Q7RB18;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative yirI protein (fragment).
 GN Name=PY06155;
 OS Plasmodium yoelii yoelii.

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angluoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Glorans L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABL01002053; EAA18316.1; -; Genomic_DNA.
DR InterPro: IPR006477; Vir_Bir_Yir; I.
DR Pfam: PF06022; Cir_Bir_Yir; I.
DR TIGRFAMs: TIGR01590; Yir-Bir-cir_Pla; 1.
FT NON TER
SQ SEQUENCE 347 AA; 40560 MW; 7D9A027871F8A7C3 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 347;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVIRVC 11
DB 31 LCKIVSHIC 40

RESULT 38
Q89DY2 BRAJA
ID Q89DY2 BRAJA PRELIMINARY; PRT; 382 AA.
AC Q89DY2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Blr7305 protein.
GN OrderedLocustNames=blr7305;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shingo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL: BAA00040; BAC52570.1; -; Genomic_DNA.
DR Complete proteome.
SQ SEQUENCE 382 AA; 42751 MW; 2F61456D78233400 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 382;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LCRIVIRVC 11
DB 83 RICEDLLARVC 93

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RESULT 39
Q960D9 DROME
ID Q960D9 DROME PRELIMINARY; PRT; 395 AA.
AC Q960D9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SD05459p.
GN ORFNames=CG8902;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY052108; AK93532.1; -; mRNA.
DR Ensemble; CG8902; Drosophila melanogaster.
DR FlyBase; FBgn0031886; CG8902.
DR GO; GO:0005252; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro: IPR003191; GBP.
SQ SEQUENCE 395 AA; 45690 MW; 402AAB1D41CE2915 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 395;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LCRIVIRVC 12
DB 66 REARVELIRVC 77

RESULT 40
Q9VM45 DROME
ID Q9VM45 DROME PRELIMINARY; PRT; 395 AA.
AC Q9VM45;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG8902-PA.
GN Names=CG8902; ORFNames=CG8902;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson X., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celinker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- INTERACTION:
CC Q86B86:CG11033; NbExp=1; IntAct=EBI-168789, EBI-105321;
CC Q9VYB1:CG9938; NbExp=1; IntAct=EBI-168789, EBI-179943;

DR EMBL; AE003616; AAF52482.2; -; Genomic_DNA.
DR IntAct; Q9VMA5; -
DR Ensembl; CG8902; Drosophila melanogaster.
DR FlyBase; FBgn0031886; CG8902.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
SQ SEQUENCE 395 AA; 45699 MW; 02801A463C7AA4C9 CRC64;
Query Match 59.7%; Score 37; DB 2; Length 395;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RLCRIVIVRVC 12
Db 66 REARVFLIRVC 77
| : : : : :
| : : : : :
RESULT 41
Q6DKZ3 TOXGO
ID Q6DKZ3_TOXGO PRELIMINARY; PRT; 553 AA.
AC Q6DKZ3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dihydrofolate/folypolyglutamate synthase (EC 6.3.2.12)
DE (EC 6.3.2.17).
GN Name=dhfs/fpgs;
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RH;
RA Smith J., Hyde J.E., Aspinall T.V., Sims P.F.G.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY669086; AAT74583.1; -; rRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008841; F:dihydrofolate synthase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004326; F:tetrahydrofolypolyglutamate synthase activity; IEA.
DR GO; GO:0003936; P:folic acid and derivative biosynthesis; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR001645; Fpolygl_synthase.
DR TIGRFAMs; TIGR01499; folC; 1.
DR PROSITE; PS01012; POLYGLUTAMATE SYNTHASE; 1.
KW Ligase.
SQ SEQUENCE 553 AA; 61388 MW; CDCF707998001D54 CRC64;
Query Match 59.7%; Score 37; DB 2; Length 553;
Best Local Similarity 58.3%; Pred. No. 3.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RLCRIVIVRVC 12
Db 238 RICKVVVVVNL 249
| : : : : :
| : : : : :
RESULT 42
Q5GA66 LYCES
ID Q5GA66_LYCES PRELIMINARY; PRT; 727 AA.
AC Q5GA66;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=56823-g5;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

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OX NCBI_TaxID=4081;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=16009996; DOI=10.1104/pp.104.058099;
RA Guyot R., Cheng X., Su Y., Cheng Z., Schlagenhauf E., Keller B.,
RA Ling H.Q.;
RT "Complex Organization and Evolution of the Tomato Pericentromeric
RT Region at the FER Gene Locus.";
RL Plant Physiol. 138:1205-1215(2005).
DR EMBL; AY678298; AAM22876.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008197; WAP.
DR InterPro; IPR000967; Znf_NFX1.
DR InterPro; IPR001965; Znf_PHD.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF01422; zf-NFX1; 7.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00438; Znf_NFX; 7.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN 1.
DR PROSITE; PSS0089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 727 AA; 80859 MW; 50CB25C831933192 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 727;
Best Local Similarity 60.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVWIRVCR 12
|||:||||
Db 358 CRLVTKSCR 367

Query Match 59.7%; Score 37; DB 2; Length 727;
Best Local Similarity 60.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 43
Q653R0_ORYSA
ID Q653R0_ORYSA PRELIMINARY; PRT; 833 AA.
AC Q653R0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein QJ1065_E04.22.
GN Names=QJ1065_E04.22;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
RT clone:OJ1065_E04.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005090; BAD45957.1; -; Genomic_DNA.
DR Gramene; Q653R0; -;
DR GO; GO:0007076; P:mitotic chromosome condensation; IEA.
DR InterPro; IPR000357; HEAT.
DR Pfam; PF02985; HEAT; 3.
KW Hypothetical protein.
SQ SEQUENCE 833 AA; 91260 MW; 7A469295E92298BA CRC64;

Query Match 59.7%; Score 37; DB 2; Length 833;
Best Local Similarity 70.0%; Pred. No. 4.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVWIRVCR 12
|||:||||
Db 814 CRKVLSEVCR 823

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RESULT 44
Q4FYML_LEIMA
ID Q4FYML_LEIMA PRELIMINARY; PRT; 934 AA.
AC Q4FYML;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LMJ_0358;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
RA Berriman M., Sisk E., Rajandream M.-A., Aert R., Anupama A.,
RA Apostolou Z., Attipoe P., Bason N., Bauser C., Beck A., Beverly S.M.,
RA Blanchettin G., Borzym K., Bothe G., Bruschi C.V., Collins M.,
RA Cadag E., Chiarloni L., Clayton C., Coulson R.M.R., Cronin A.,
RA Cruz A.K., Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
RA Pazelina G., Fosker N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
RA Goble A., Goffeau A., Harris D., Hertz-Powler C., Hilbert H., Horn D.,
RA Huang Y., Klages S., Knights A., Kube M., Larke N., Litvin L.,
RA Lord A., Louie T., Marra M., Masuy D., Matthews K., Michaeli S.,
RA Mottram J.C., Muller-Auer S., Munden H., Nelson S., Norbertczak H.,
RA Oliver K., O'Neill S., Pentony M., Pohl T.M., Price C., Purnelle B.,
RA Quail M.A., Rabinowitsch E., Reinhardt R., Rieger M., Rinta J.,
RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D., Sharp S.,
RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,
RA Volckaert G., Wambutt R., Warren T., Wedler H., Woodward J., Zhou S.,
RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
RA Myler P.J.;
RT "The genome of the kinetoplastid parasite, Leishmania major.";
RL Science 0:0-0(2005).
DR EMBL; CP000079; AAZ09847.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 934 AA; 104791 MW; CB93E681238D3828 CRC64;

Query Match 59.7%; Score 37; DB 2; Length 934;
Best Local Similarity 63.6%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIWIRVVC 11
|||||
Db 464 RLCRCATITVC 474

RESULT 45
Q5B248_EMENI
ID Q5B248_EMENI PRELIMINARY; PRT; 320 AA.
AC Q5B248;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN5381.2, AN5382.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collumore A., Cooke A., Cooke P., Corum B., DeArelano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,

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DR EMBL; U00016; AAA17163.1; -; Genomic_DNA.
DR EMBL; Z99125; CAB16145.1; -; Genomic_DNA.
DR PIR; S72595; S72595.
KW Hypothetical protein.
SQ SEQUENCE 165 AA; 18436 MW; CCCB97CC64D9031 CRC64;

Query Match      58.1%; Score 36; DB 2; Length 165;
Best Local Similarity 58.3%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LCRIVVIRVCR 12
    |||:|
Db 62 RLQQLGSDRVC 73

RESULT 49
Q4SWCO_TETNG
ID Q4SWCO_TETNG PRELIMINARY; PRT; 166 AA.
AC Q4SWCO_TETNG
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAFI3636, whole genome shotgun sequence.
DE (Fragment).
ORFNames=GSTENG0001158001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat G., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
RA Kallis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01013636; CAF95062.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 166 AA; 18832 MW; 9FEF0F5D8337E327 CRC64;

Query Match      58.1%; Score 36; DB 2; Length 166;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LCRIVVIRVCR 12
    |||:|
Db 134 LCRITINRVAR 144

RESULT 50
Q5UNZ4_MIMIV
ID Q5UNZ4_MIMIV PRELIMINARY; PRT; 181 AA.
AC Q5UNZ4_MIMIV
DT 01-FEB-2005 (TrEMBLrel. 29, Created)

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DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MIMI_R744;
OS Mimivirus.
OC Viruses; dsDNA viruses, no RNA stage; Mimivirus.
OX NCBI_TaxID=212035;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX MEDLINE=22550848; PubMed=12663918; DOI=10.1126/science.1081867;
RA La Scola B., Audic S., Robert C., Jungang L., de Lamballerie X.,
RA Drancourt M., Birtles R., Claverie J.M., Raoult D.;
RT "A giant virus in amoebae.";
RL Science 299:2033-2033(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX PubMed=15486256; DOI=10.1126/science.1101485;
RA Raoult D., Audic S., Robert C., Abergel C., Renesto P., Ogata H.,
RA La Scola B., Susan M., Claverie J.M.;
RT "The 1.2-Mb Genome Sequence of Mimivirus.";
RL Science 306:1344-1350(2004).
DR EMBL; AY653733; AAV51004.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 181 AA; 21726 MW; E4250CFDBFC66E20 CRC64;

Query Match      58.1%; Score 36; DB 2; Length 181;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVVIRVCR 11
    ||:| :|:|
Db 125 LCKICLVKIC 134

RESULT 51
Q9A9J3_CAUCR
ID Q9A9J3_CAUCR PRELIMINARY; PRT; 219 AA.
AC Q9A9J3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CC0987.
GN OrderedLocusNames=CC0987;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Emolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005776; AAK22971.1; -; Genomic_DNA.
DR PIR; G87371; G87371.
DR TIGR; CC0987; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 219 AA; 22879 MW; 6BF59EE9625F54EF CRC64;

Query Match      58.1%; Score 36; DB 2; Length 219;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 RLCRIVVIRVC 11
      |||:::|
Db      174 RCCRVIQARLC 184

RESULT 52
ID Q9QJ35_9BETA PRELIMINARY; PRT; 276 AA.
AC Q9QJ35;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE U34.
GN Name=U34;
OS Human herpesvirus 6B.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OK NCBI_TaxID=32604;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Z29;
RX MEDLINE=99412318; PubMed=10482553;
RA Dominguez G., Dambaugh T.R., Stamey F.R., Dewhurst S., Inoue N.,
RA Pellett P.E.;
RT "Human herpesvirus 6B genome sequence: coding content and comparison
RT with human herpesvirus 6A.";
RL J. Virol. 73:8040-8052(1999).
DR EMBL; AF157706; AAD49648.1; -; Genomic_DNA.
DR InterPro; IPR007626; Herpes_U34.
DR Pfam; PF04541; Herpes_U34; 1.
SQ SEQUENCE 276 AA; 31440 MW; FA1956D7BEBB85A CRC64;

Query Match 58.1%; Score 36; DB 2; Length 276;
Best Local Similarity 36.4%; Pred. No. 2.6e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVC 11
      |||:::|
Db      242 RHCRAIVSIC 252

RESULT 53
ID Q9WT30_9BETA PRELIMINARY; PRT; 276 AA.
AC Q9WT30;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Virion protein.
GN Name=U34;
OS Human herpesvirus 6B.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OK NCBI_TaxID=32604;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HST;
RX MEDLINE=99412319; PubMed=10482554;
RA Isegawa Y., Mukai T., Nakano K., Kagawa M., Chen J., Mori Y.,
RA Sunagawa T., Kawanishi K., Sashihara J., Hata A., Zou P., Kosuge H.,
RA Yamanishi K.;
RT "Comparison of the complete DNA sequences of human herpesvirus 6
RT variants A and B.";
RL J. Virol. 73:8053-8063(1999).
DR EMBL; AB021506; BAA78255.1; -; Genomic_DNA.
DR PIR; T43994; T43994.
DR InterPro; IPR007626; Herpes_U34.
DR Pfam; PF04541; Herpes_U34; 1.
SQ SEQUENCE 276 AA; 31526 MW; 550EC78160E3790C CRC64;

Query Match 58.1%; Score 36; DB 2; Length 276;
Best Local Similarity 36.4%; Pred. No. 2.6e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVC 11
      |||:::|
Db      242 RHCRAIVSIC 252

RESULT 54
ID Q7RSR4_GIALA PRELIMINARY; PRT; 316 AA.
AC Q7RSR4;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE GLP 487 15862 14912.
OS Giardia_lambia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OK NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000004; EAA42578.1; -; Genomic_DNA.
SQ SEQUENCE 316 AA; 35086 MW; 1357988CCF7D9CB3 CRC64;

Query Match 58.1%; Score 36; DB 2; Length 316;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      3 CRIVVIRVC 12
      |||:::|
Db      141 CEVTEIRICR 150

RESULT 55
ID Q5L9S8_BACFN PRELIMINARY; PRT; 328 AA.
AC Q5L9S8;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Putative LPS biosynthesis related glycosyltransferase.
GN OrderedLocustNames=BF3458;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OK NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression.";
RL Science 307:1463-1465(2005).
DR EMBL; CR626927; CAH09149.1; -; Genomic_DNA.
DR InterPro; IPR001173; Glyco_transf.2.
DR Pfam; PF00535; Glycos_transf.2; 1.
KW Complete proteome; Transference.
SQ SEQUENCE 328 AA; 38246 MW; 61B3BCA2669F0038 CRC64;

Query Match 58.1%; Score 36; DB 2; Length 328;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY      1 LRCRIIVIRVC 12
DB      284 RICRIIVTFYKCK 295

RESULT 56
Q9XU00.CABEL
ID      Q9XU00_CABEL PRELIMINARY; PRT; 344 AA.
AC      Q9XU00;
DT      01-NOV-1999 (TrEMBLrel. 12, Created)
DT      01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Hypothetical protein K06G5.3.
GN      ORFNames=K06G5.3;
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=Bristol N2;
RX      MEDLINE=99069613; PubMed=9851916;
RG      The C. elegans sequencing consortium;
RT      "Genome sequence of the nematode C. elegans: a platform for
RT      investigating biology.";
RL      Science 282:2012-2018(1998).
DR      EMBL; Z81565; CAB04580.1; -; Genomic_DNA.
DR      PIR; T23374; T23374.
DR      Ensembl; K06G5.3; Caenorhabditis elegans.
DR      WormBase; WBGene00010607; K06G5.3.
DR      WormPep; K06G5.3; CE18853.
DR      Complete proteome; Hypothetical protein.
SQ      SEQUENCE 344 AA; 37804 MW; A3DJA8E8C5CC2194 CRC64;

Query Match      58.1%; Score 36; DB 2; Length 344;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 LCRIVIRVC 11
DB      55 LCBIIVSKIC 64

RESULT 57
Q8L535_ORYSA
ID      Q8L535_ORYSA PRELIMINARY; PRT; 364 AA.
AC      Q8L535;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE      Hypothetical protein OSJNBb0072F04.13 (Hypothetical protein
DE      OSJNBb0072F04.7).
GN      Name=OSJNBb0072F04.7; ORFNames=OSJNBb0072F04.13;
OS      Oryza sativa (japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzoae; Oryza.
OX      NCBI_TaxID=39947;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA      Sasaki C., Henry D., Oates R., Simmons J.;
RA      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL      [2]
RN      NUCLEOTIDE SEQUENCE.
RC      Wing R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R.,
RA      Rambo T., Sasaki C., Henry D., Oates R., Simmons J.;
RA      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL      [3]
RN      NUCLEOTIDE SEQUENCE.
RC      The Rice Chromosome 10 Sequencing Consortium;
RA      "In-depth view of structure, activity, and evolution of rice
RT      chromosome 10.";

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RL      Science 300:1566-1569(2003).
RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RC      Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RA      Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL      EMBL; AC092553; AAM23247.1; -; Genomic_DNA.
DR      EMBL; AC122147; AAM47618.1; -; Genomic_DNA.
DR      EMBL; AE017053; AAP51985.1; -; Genomic_DNA.
DR      Gramene; Q8L535; -.
KW      Hypothetical protein.
SQ      SEQUENCE 364 AA; 40276 MW; 2620285B852A706E CRC64;

Query Match      58.1%; Score 36; DB 2; Length 364;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 LRCRIIVIRVC 11
DB      162 LRCRIVLDLC 172

RESULT 58
Q8T206_DICDI
ID      Q8T206_DICDI PRELIMINARY; PRT; 379 AA.
AC      Q8T206;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE      Hypothetical protein.
GN      ORFNames=DD50217597;
OS      Dictyostelium discoideum (Slime mold).
OC      Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX      NCBI_TaxID=44689;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=AX4;
RC      Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA      Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA      Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT      "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=AX4;
RC      Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA      Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA      Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA      Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA      Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA      Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA      Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA      Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA      Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA      Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA      Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA      Loubegeh H., Mungall K., Oliver K., Price C., Quail M.A.,
RA      Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA      Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA      Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA      Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA      Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA      Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT      "The genome of the social amoeba Dictyostelium discoideum.";
RL      Nature 0:0-0(2005).
RN      EMBL; AC116305; AAL92250.1; -; Genomic DNA.
DR      EMBL; AAFI01000028; EAL69898.1; -; Genomic DNA.
DR      GO; GO:0016740; Ftransferase activity; IEA.
DR      GO; GO:0008654; Pphospholipid biosynthesis; IEA.
DR      InterPro; IPR000462; CDP-OH_P_trans.
DR      Pfam; PF01066; CDP-OH_P_transf; 1.
DR      PROSITE; PS00379; CDP_ALCOHOL_P_TRANSF; 1.
KW      Hypothetical protein; Transferase.
SQ      SEQUENCE 379 AA; 43303 MW; D5267F8CC7F95ABE CRC64;

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Query Match 58.1%; Score 36; DB 2; Length 379;
 Best Local Similarity 45.5%; Pred. No. 3.6e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 12
 Db 288 VRCIVQRICQ 298
 :||:|:|:
 288 VRCIVQRICQ 298

RESULT 59
 EPTI YEAST STANDARD; PRT; 391 AA.
 AC P22140;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ethanolaminephosphotransferase (EC 2.7.8.1) (ETHPT)
 GN Name=EPTI; OrderedLocNames=YHR123W;
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OK NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DBY746;
 RX MEDLINE=91161601; PubMed=1848238;
 RA Hjelmstad R.H., Bell R.M.;
 RT "sn-1,2-diacylglycerol choline- and ethanolaminephosphotransferases in
 RT Saccharomyces cerevisiae. Nucleotide sequence of the EPTI gene and
 RT comparison of the CPT1 and EPT1 gene products.";
 RL J. Biol. Chem. 266:5094-5103(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=S288c / AB972;
 RX MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 RA Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
 RA Lareelle P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
 RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaaskis E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VIII.";
 RL Science 265:2077-2082(1994).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=91154238; PubMed=1847919;
 RA Hjelmstad R.H., Bell R.M.;
 RT "sn-1,2-diacylglycerol choline- and ethanolaminephosphotransferases in
 RT Saccharomyces cerevisiae. Mixed micellar analysis of the CPT1 and EPT1
 RT gene products.";
 RL J. Biol. Chem. 266:4357-4365(1991).
 CC -1- FUNCTION: Involved in protein-dependent process of phospholipid
 CC transport to distribute phosphatidyl ethanolamine to the luminal
 CC surface. The multiple transmembrane domains and luminal
 CC hydrophilic domains of the ethanolaminephosphotransferase might
 CC participate in the transport process. EPT1 catalyzes both choline-
 CC and ethanolamine-phosphotransferase reactions.
 CC -1- CATALYTIC ACTIVITY: CDP-ethanolamine + 1,2-diacylglycerol = CMP +
 CC a phosphatidylethanolamine.
 CC -1- PHOSPHATYLACTIVITY: CDP-choline + 1,2-diacylglycerol = CMP + a
 CC phosphatidylcholine.
 CC -1- COFACTOR: Phospholipid.
 CC -1- ENZYME REGULATION: Requires a divalent cation activator, and is
 CC inhibited by CMP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Microsomal
 CC vesicles.
 CC -1- SIMILARITY: Belongs to the CDP-ethanolamine phosphatidyltransferase
 CC class-I family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

CC EMBL; M59311; AAA63572.1; -; Genomic DNA.
 CC EMBL; U10398; AAB68409.1; -; Genomic DNA.
 CC PIR; S48967; S48967.
 CC GeneOnline; 139440; -;
 CC Ensembl; YHR123W; Saccharomycetes cerevisiae.
 CC SGD; S000001165; EPT1.
 CC InterPro; IPR000462; CDP-OH P trans.
 CC Pfam; PF01066; CDP-OH P trans; 1.
 CC PROSITE; PS00379; CDP-ALCOHOL P TRANSF; 1.
 KW Complete proteome; Endoplasmic reticulum; Membrane; Microsome;
 KW Multifunctional enzyme; Phospholipid biosynthesis; Transferase;
 KW Transmembrane.
 FT TOPO_DOM 1 48 Luminal (Potential).
 FT TRANSMEM 49 69 Potential.
 FT TOPO_DOM 70 174 Cytoplasmic (Potential).
 FT TRANSMEM 175 195 Potential.
 FT TRANSMEM 216 236 Potential.
 FT TRANSMEM 263 283 Potential.
 FT TRANSMEM 289 309 Potential.
 FT TRANSMEM 319 339 Potential.
 FT TRANSMEM 347 367 Potential.
 FT TOPO_DOM 368 391 Cytoplasmic (Potential).
 FT CONFLICT 96 96 D -> V (in Ref. 1).
 FT CONFLICT 98 98 C -> S (in Ref. 1).
 SQ SEQUENCE 391 AA; 44560 MW; 038942A7FB9EB580 CRC64;

Query Match 58.1%; Score 36; DB 1; Length 391;
 Best Local Similarity 50.0%; Pred. No. 3.7e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 11
 Db 327 LCQIVLYKIC 336
 :||:|:|:
 327 LCQIVLYKIC 336

RESULT 60
 Q9V5B0 DROME
 ID Q9V5B0 DROME PRELIMINARY; PRT; 446 AA.
 AC Q9V5B0; Q95SK9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE CG1776-PA (GH17420p).
 DE ORFNames=CG1776;
 GN Drosophila melanogaster (Fruit fly).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OK NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Claway S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupay J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "*Drosophila melanogaster* release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RA Stapleton M., Brokatein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF003832; AAF58906.3; -; Genomic_DNA.
DR EMBL; AY060726; AAL28274.1; -; mRNA.
DR HSSP; P49137; INY3.
DR Ensembl; CG1776; Drosophila melanogaster.
DR FlyBase; FBgn0033441; CG1776.
DR GO; GO:0007015; P:actin filament organization; IMP.
DR GO; GO:0008360; P:regulation of cell shape; IMP.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 446 AA; 5082 MW; D9ED201F7896A2B4 CRC64;
Query Match 58.1%; Score 36; DB 2; Length 446;
Best Local Similarity 45.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 RLCRIVVIRVC 11
|:|:|:|:|:
DB 130 RVCRVFIRQVC 140
RESULT 61
Q7F803_ORYSA
ID Q7F803_ORYSA PRELIMINARY; PRT; 708 AA.
AC Q7F803;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to Arabidopsis thaliana chromosome V FI MJJ3; MJJ3.6.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002539; BAB08195.2; -; Genomic_DNA.
DR Gramene; Q7F803; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR006058; 2Fe2S fd_BS.
DR InterPro; IPR000967; Znf_NFX1.
DR InterPro; IPR001965; Znf_PHD.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF01422; zf-NFX1; 5.
DR SMART; SM00438; Znf_NFX; 7.
DR PROSITE; PS00197; 2FE2S FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS01359; ZF_PHD 1; UNKNOWN_1.
DR PROSITE; PS50089; ZF_RING_2; 1.

KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 708 AA; 77564 MW; C886DA2B927FC928 CRC64;

Query Match 58.1%; Score 36; DB 2; Length 708;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVVIRVCR 12
| : | : | : |
Db 387 CRLVITKSCR 396

RESULT 62
Q805B9 BRARE
ID Q805B9 BRARE PRELIMINARY; PRT; 815 AA.
AC Q805B9
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Fibroblast growth factor receptor 2b precursor.
GN Name=fgfr2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Tonou-Fujimori N., Takahashi M., Onodera H., Kikuta H., Koshida S.,
RA Takeda H., Yamasu K.;
RT "Expression of the FGF receptor 2 gene (fgfr2) during embryogenesis in
RT the zebrafish Danio rerio.";
RL Gene Expr. Patterns 2:183-188(2002).
DR EMBL; AB094118; BAC35011.1; -; mRNA.
DR HSSP; Q9UQH9; IGJO.
DR SMR; Q805B9; 152-359, 461-757.
DR Ensembl; ENSDARG0000004811; Danio rerio.
DR ZFIN; ZDB-GENE-030323-1; fgfr2.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor; Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 815 AA; 91146 MW; A3A5DF12020F2AE3 CRC64;

Query Match 58.1%; Score 36; DB 2; Length 815;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVVIRVCR 12
| : | : | : |
Db 388 CMVVIVVVCRC 397

RESULT 63
Q805B9 BRARE
ID Q805B9 BRARE PRELIMINARY; PRT; 815 AA.
AC Q805B9
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Fibroblast growth factor receptor 2b precursor.
GN Name=fgfr2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Tonou-Fujimori N., Takahashi M., Onodera H., Kikuta H., Koshida S.,
RA Takeda H., Yamasu K.;
RT "Expression of the FGF receptor 2 gene (fgfr2) during embryogenesis in
RT the zebrafish Danio rerio.";
RL Gene Expr. Patterns 2:183-188(2002).
DR EMBL; AB094118; BAC35011.1; -; mRNA.
DR HSSP; Q9UQH9; IGJO.
DR SMR; Q805B9; 152-359, 461-757.
DR Ensembl; ENSDARG0000004811; Danio rerio.
DR ZFIN; ZDB-GENE-030323-1; fgfr2.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor; Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 815 AA; 91146 MW; A3A5DF12020F2AE3 CRC64;

Query Match 58.1%; Score 36; DB 2; Length 815;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVVIRVCR 12
| : | : | : |
Db 388 CMVVIVVVCRC 397

RESULT 64
Q805B9 BRARE
ID Q805B9 BRARE PRELIMINARY; PRT; 817 AA.
AC Q805B9
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Fibroblast growth factor receptor 2.
GN Name=fgfr2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Tonou-Fujimori N., Takahashi M., Onodera H., Kikuta H., Koshida S.,
RA Takeda H., Yamasu K.;
RT "Expression of the FGF receptor 2 gene (fgfr2) during embryogenesis in
RT the zebrafish Danio rerio.";
RL Gene Expr. Patterns 2:183-188(2002).
DR EMBL; AB084105; BAC20194.1; -; mRNA.
DR HSSP; Q9UQH9; IGJO.
DR SMR; Q805B9; 152-362, 461-757.
DR Ensembl; ENSDARG0000004811; Danio rerio.
DR ZFIN; ZDB-GENE-030323-1; fgfr2.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; Ig; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 815 AA; 91243 MW; 9E6D4D1CFEF6D56C CRC64;

Query Match 58.1%; Score 36; DB 2; Length 815;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVVIRVCR 12
| : | : | : |
Db 390 CMVVIVVVCRC 399

Submitted (APR-2001) to the EMBL/GenBank/DDSIJ databases.

EMBL; AJ309303; CAC84705.1; -, mRNA.

HSSP; Q9U0H9, 1GJO.

SMR; Q8JG38, 152-362, 463-759.

Ensembl; ENSDARG0000004811; Danio rerio.

ZFIN; ZDB-GENE-030323-1; igf1r2.

GO; GO:0016021; C-integral to membrane; IEA.

GO; GO:0005524; F-ATP binding; IEA.

GO; GO:0004713; F-protein-tyrosine kinase activity; IEA.

GO; GO:0004872; F-receptor activity; IEA.

GO; GO:0016740; F-transferase activity; IEA.

GO; GO:0006468; F-protein amino acid phosphorylation; IEA.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig c2.

InterPro; IPR000719; Prot_kinase.

InterPro; IPR001245; Tyr_kinase.

InterPro; IPR008266; Tyr_kinase_AS.

Pfam; PF00047; ig; 2.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00408; IGC2; 3.

SMART; SM00219; TyrKc; 1.

PROSITE; PS50835; IG LIKE; 3.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

Receptor.

SW
SEQUENCE 817 AA; 91388 MW; 0A6D9F5412B27D69 CRC64;

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Query Match      58.1%; Score 36; DB 2; Length 817;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels

QY      3 CRIVWIRVCR 12
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Db      390 CMWIVVWVCR 399

```

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RESULT 65
QB05Q4_9RETR
ID QB05Q4_9RETR PRELIMINARY; PRT; 853 AA.
AC QB05Q4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope polyprotein.
GN Name=env;
OS Feline immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Feline lentiviruses.
OX NCBI_TaxID=11673;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Harmache A., Meiring C., Learn G.H. Jr., Hoover E.A., Mullins J.I.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF474246; AAM13447.1; -; Genomic_RNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002050; Env_polyprotein.
DR Pfam; PF00429; TIV_coat; 1.
DR Envelope protein; Polyprotein.
SQ SEQUENCE 853 AA; 98201 MW; D0EE32196AA3DDC1 CRC64;

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Query Match      58.1%; Score 36; DB 2; Length 853;
Best Local Similarity 54.5%; Pred. No. 7.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels

Qy      1 RLCRIWVRVC 11
      | | | | | | |
Db      146 RNCRIITAIIC 156

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RESULT 66

Q6FXG3_CANGA

ID Q6FXG3_CANGA PRELIMINARY; PRT; 856 AA.

AC Q6FXG3;

DT 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Similar to tr|Q06479 Saccharomyces cerevisiae YLR352w.

GN OrderedLocusNames=CAGL0B03113g;

OC Candida glabrata (Yeast) (Torulopsis glabrata).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI_TaxID=5478;

[1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP STRAIN=ATCC 2001 / CBS 138;

RC PubMed=15229592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E.,

RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

RA Boismase A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,

RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

RA Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,

RA Swennen D., Tekaiia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

RA Zeniou-Meyer M., Zivanovic B., Bolotin-Fukuhara M., Thierry A.,

RA Bouchier C., Caudron B., Scarpeilli C., Gaillardin C., Weissenbach J.,

RA Wincker P., Souciet J.-L.;

RT "Genome evolution in yeasts.";

RL Nature 430:35-44(2004).

DR EMBL; CR380948; CAG58008.1; -; Genomic_DNA.

DR InterPro; IPR07089; LRR_cys.

SW Complete proteome.

SQ SEQUENCE 856 AA; 98009 MW; C0AD0DBA3DE9E089 CRC64;

```

Query Match      58.1%; Score 36; DB 2; Length 956;
Best Local Similarity 50.0%; Pred. NO. 7.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 LCRIVWIRVC 11
      :||:|
Db      61 ICRVLVRYC 70

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RESULT 67

ID	Q5ZEL8_ORYSA PRELIMINARY;	PRT;	909 AA.
Q5ZEL8;			
DC	25-OCT-2004 (TrEMBLrel. 28, Created)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Hypotheoretical protein P0041E11.9.		
GN	Names=P0041E11.9;		
OS	Oryza sativa (japonica cultivar-group) .		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Oryzeae; Oryza.		
OX	NCBI_Taxid=39947;		
RX	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,		
RA	Wu J., Nimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,		
RA	Hosokawa S., Masukawa M., Arioka K., Chiden Y., Hayashi M.,		
RA	Okamoto M., Ando T., Aoki H., Arita K., Hanada M., Harada C.,		
RA	Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,		
RA	Ikeno M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,		
RA	Karasaawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,		
RA	Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,		
RA	Nagaasaki H., Nakashima M., Nakama Y., Nakanishi Y., Nakamura M.,		
RA	Namiki N., Negishi M., Ohta I., Ono N., Saij S., Sakai K., Shibata M.,		

RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojibori T.,
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP002521; BAD61082.1; -; Genomic_DNA.
DR Gramene; Q5ZEL8; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR006058; 2Fe2S_fld_BS.
DR InterPro; IPR000967; Znf_NFX1.
DR InterPro; IPR001965; Znf_PHD.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF01422; zf-NFX-X1; 10.
DR SMART; SM00438; Znf_NFX; 11.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 909 AA; 99556 MW; 463938DD12E2CA11 CRC64;

Query Match 58.1%; Score 36; DB 2; Length 909;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
Db 387 CRLVITKSCR 396
||:|:|:|

RESULT 68
Q7PVF3 ANOGA
ID Q7PVF3 ANOGA PRELIMINARY; PRT; 1284 AA.
AC Q7PVF3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000010651 (Fragment).
GN ORFNames=ENSG000000008162;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR EMBL; AAB01008984; EAA15114.2; -; Genomic DNA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR003877; SPRY_receptor.

DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
FT NON TER 1
SQ SEQUENCE 1284 AA; 144060 MW; 9130A53FCD4C7183 CRC64;

Query Match 58.1%; Score 36; DB 2; Length 1284;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
Db 1257 CKLIIRVTR 1266
||:|:|:|

RESULT 69
Q59DX2 DROME
ID Q59DX2 DROME PRELIMINARY; PRT; 1357 AA.
AC Q59DX2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG33555-PA, isoform A.
GN Name=btaz; ORFNames=CG33555;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Chen B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G.,
RA Palazolo M., Pittman G.S., Fan S., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.H., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";


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RL Science 287:2185-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celnikier S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 C2 domains.
DR EMBL; AE003706; AAX52952.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
SQ SEQUENCE 1357 AA; 149802 MW; D8B981B9F9A89066 CRC64;

Query Match 58.1%; Score 36; DB 2; Length 1357;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVTVTRVC 12
DB 45 CRVCKLRVCK 54

RESULT 70
Q4YRN6_PLABE
ID Q4YRN6_PLABE PRELIMINARY; PRT; 472 AA.
AC Q4YRN6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Dihydrofolate synthase/folylpolyglutamate synthase, putative.
GN ORFNames=PB000177.03.0;

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OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN NCBI_TaxID=5821;
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86 (2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAI01002742; CAH99321.1; -; Genomic_DNA.
SQ SEQUENCE 472 AA; 53985 MW; 84EF97DA2065D9A6 CRC64;

Query Match 57.3%; Score 35.5; DB 2; Length 472;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

QY 1 RLCRIV-----VIRVC 11
DB 310 RLCRDVNCFHFKDKIIRVC 327

RESULT 71
Q19522_CASEL
ID Q19522_CASEL PRELIMINARY; PRT; 2761 AA.
AC Q19522; Q20718;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein F53B7.5.
GN ORFNames=F53B7.5;
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018 (1998).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Bristol N2;
RA McMurray A.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z72510; CAA96654.1; -; Genomic_DNA.
DR EMBL; Z72507; CAA96634.1; -; Genomic_DNA.
DR EMBL; Z72510; CAA96654.1; JOINED; Genomic_DNA.
DR EMBL; Z72510; CAA96634.1; JOINED; Genomic_DNA.
DR PIR; T21064; T21064.
DR Ensembl; F53B7.5; Caenorhabditis elegans.
DR WormBase; WSGene0009968; F53B7.5.
DR WormPep; F53B7.5; CE05924.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002601; C6.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR000884; TSPL.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01681; C6; 18.
DR Pfam; PF00090; TSP_1; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN 1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.

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DR PROSITE; PS00092; TSF1; 1.
KW PROSITE; PS00678; WD REPEATS 1; UNKNOWN_1.
KW Complete proteome; Hypothetical protein_
SQ SEQUENCE 2761 AA; 282476 MW; DD368C3477A73068 CRC64;

Query Match 57.3%; Score 35.5; DB 2; Length 2761;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CRIVVIRVCR 12
Db 2472 CRIVVIRVCR 2480

RESULT 72
Q60MN8 CAEBR
ID Q60MN8 CAEBR PRELIMINARY; PRT; 3008 AA.
AC Q60MN8;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein CBG23067.
GN Name=CBG23067;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100041; CAE75138.1; -; Genomic_DNA.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR002601; C6.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR000884; TSF1.
DR Pfam; PF01681; C6; 18.
DR Pfam; PF00090; TSF_1; 2.
DR SMART; SMO0209; TSF1; 2.
DR PROSITE; PS00061; ADH SHORT; UNKNOWN_1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00092; TSF1; 2.
KW Hypothetical protein.
SQ SEQUENCE 3008 AA; 311802 MW; 3C082C2FD961DF5D CRC64;

Query Match 57.3%; Score 35.5; DB 2; Length 3008;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CRIVVIRVCR 12
Db 2524 CRIVVIRVCR 2532

RESULT 73
Q731N5 BACCI
ID Q731N5 BACCI PRELIMINARY; PRT; 38 AA.
AC Q731N5;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BCE4130;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]

DR PROSITE; PS00092; TSF1; 1.
KW PROSITE; PS00678; WD REPEATS 1; UNKNOWN_1.
KW Complete proteome; Hypothetical protein_
SQ SEQUENCE 2761 AA; 282476 MW; DD368C3477A73068 CRC64;

Query Match 57.3%; Score 35.5; DB 2; Length 2761;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CRIVVIRVCR 12
Db 2472 CRIVVIRVCR 2480

RESULT 72
Q60MN8 CAEBR
ID Q60MN8 CAEBR PRELIMINARY; PRT; 3008 AA.
AC Q60MN8;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein CBG23067.
GN Name=CBG23067;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100041; CAE75138.1; -; Genomic_DNA.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR002601; C6.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR000884; TSF1.
DR Pfam; PF01681; C6; 18.
DR Pfam; PF00090; TSF_1; 2.
DR SMART; SMO0209; TSF1; 2.
DR PROSITE; PS00061; ADH SHORT; UNKNOWN_1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00092; TSF1; 2.
KW Hypothetical protein.
SQ SEQUENCE 3008 AA; 311802 MW; 3C082C2FD961DF5D CRC64;

Query Match 57.3%; Score 35.5; DB 2; Length 3008;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CRIVVIRVCR 12
Db 2524 CRIVVIRVCR 2532

RESULT 73
Q731N5 BACCI
ID Q731N5 BACCI PRELIMINARY; PRT; 38 AA.
AC Q731N5;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BCE4130;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Pouts D.E., Tourasse N.J., Angluoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017277; AAS43032.1; -; Genomic_DNA.
DR TIGR; BCE4130; -.
KW Complete proteome.
SQ SEQUENCE 38 AA; 4353 MW; BA0C689ACFC36F56 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 38;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IVVIRVCR 12
Db 30 VIVVIRICR 37

RESULT 74
Q6IMS1 DROME
ID Q6IMS1 DROME PRELIMINARY; PRT; 131 AA.
AC Q6IMS1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE HDC07475.
GN ORFNames=HDC07475;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
RA Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
RA Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001815; DAA02659.1; -; Genomic DNA.
DR EMBL; BK001815; DAA02659.1; -; Genomic DNA.
SQ SEQUENCE 131 AA; 14414 MW; 21EAE72089AA9A7A CRC64;

Query Match 56.5%; Score 35; DB 2; Length 131;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVCR 12
Db 64 CRVSGVRVCK 73

RESULT 75
Q9EX49 STRCO
ID Q9EX49 STRCO PRELIMINARY; PRT; 134 AA.
AC Q9EX49;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein SCO0989.
GN OrderedLocNames=SCO0989; ORFNames=2SCG2.02c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
RL EMBL; ALG9107; CAC14357.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 134 AA; 14136 MW; 92A346DE3135F0BD CRC64;

Query Match 56.5%; Score 35; DB 2; Length 134;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVWIRVC 11
|||:|:|
DB 24 CRVVVCRDC 32

RESULT 76
Q64S75_BACFR PRELIMINARY; PRT; 214 AA.
ID Q64S75_BACFR PRELIMINARY;
AC Q64S75;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Serine type site-specific recombinase.
GN OrderedLocuNames=SF2906;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RA "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924 (2004).
DR EMBL; AP006841; BAD49655.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 214 AA; 24309 MW; 9D21F9C533DCAC62 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 214;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVWIRV 10
|||:|:|
DB 78 LCRIVWIRV 86

RESULT 77
Q4LIU4_9BURK PRELIMINARY; PRT; 225 AA.
ID Q4LIU4_9BURK PRELIMINARY;
AC Q4LIU4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Ecen2424DRAFT_0677;
OS Burkholderia cenocepacia H12424.

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OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW EMBL; A4HL0100078; EAM15965.1; -; Genomic_DNA.
SQ SEQUENCE 225 AA; 24198 MW; 9AF17E944B3E85B9 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 225;
Best Local Similarity 43.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 1 RLCRIVWIRV----VCR 12
:|:|:|:|
DB 24 KLCDLVILRGSTVVC 39

RESULT 78
Q8DWC3_STRMU PRELIMINARY; PRT; 233 AA.
ID Q8DWC3;
AC Q8DWC3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein SMU.141.
GN OrderedLocuNames=SMU.141;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UAI59 / ATCC 700610 / Serotype c;
RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL; AE014866; AAN57920.1; -; Genomic_DNA.
DR InterPro; IPR010699; DUF1275.
DR Pfam; PF06912; DUF1275; 1.
KW Complete proteome.
SQ SEQUENCE 233 AA; 25992 MW; F7BBF61ABF61DF18 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 233;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LCRIVWIRVC 11
|||:|:|
DB 213 LCEIIIFTVC 222

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RESULT 79
Q57M2_HUMAN
ID Q57M2_HUMAN PRELIMINARY; PRT; 234 AA.
AC Q57M2;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 18.
GN Name=TNFRSF18; ORFNames=RP5-902P8.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Harrison E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162741; CAI23248.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 234 AA; 25110 MW; 55DB593CD0B1DB45 CRC64;
Query Match 56.5%; Score 35; DB 2; Length 234;
Best Local Similarity 50.0%; Pred. No. 3.4e-02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVCR 12
Db 48 RCRVHTTRCCR 59

RESULT 80
TNR18_HUMAN
ID TNR18_HUMAN STANDARD; PRT; 241 AA.
AC Q9Y5U5; Q9Y581; Q9NVJ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE TNFR family receptor).
GN Name=TNFRSF18; Synonyms=A1TR, G1TR; ORFNames=UNQ319/PRO364;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND INTERACTIONS WITH TRAF1; TRAF2
RP AND TRAF3.
RC TISSUE=Bone marrow;
RX MEDLINE=99175482; PubMed=10074428; DOI=10.1016/S0960-9822(99)80093-1;
RA Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T.,
RA Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
RA Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
RA Ashkenazi A.;
RA "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 9:215-218(1999).
[2]
RN RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=T-cell;
RX MEDLINE=99156876; PubMed=10037686; DOI=10.1074/jbc.274.10.6056;
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
RA Liu D., Wang S.-X., Kwon B.S.;
RA "Identification of a novel activation-inducible protein of the tumor
RT necrosis factor receptor superfamily and its ligand.";
RL J. Biol. Chem. 274:6056-6061(1999).
[3]
RN RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847; DOI=10.1038/sj.cdd.4400670;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 7:408-410(2000).
[4]
RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wicand D., Woods K., Xie M.-H., Goddard A.D.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[5]
RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
[6]
RN RP PROTEIN SEQUENCE OF 26-40.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RL verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC interactions between activated T lymphocytes and endothelial cells
CC and in the regulation of T cell receptor-mediated cell death.
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
CC TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2; Synonyms=G1TR-D;
CC IsoId=Q9Y5U5-1; Sequence=Displayed;
CC -!- TISSUE SPECIFICITY: Expressed in lymph node, peripheral blood
CC leukocytes and weakly in spleen.
CC -!- INDUCTION: Up-regulated in peripheral mononuclear cells after
CC antigen stimulation/lymphocyte activation.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF125304; AAD22635.1; -; mRNA.
CC EMBL; AF117297; AAD19694.1; -; mRNA.
CC EMBL; AF241229; AAF63506.1; -; mRNA.
CC EMBL; AY358877; AAQ89236.1; -; mRNA.
CC EMBL; BT019532; AAV38339.1; -; mRNA.
CC EMBL; ENSG00000186891; Homo sapiens.
CC HGNC; HGNC:11914; TNFRSF18.
CC MIM; 603905; -.
CC GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.

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DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001368; TNFR_C6
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS00650; TNFR_NGFR_2; FALSE NEG.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 241 Tumor necrosis factor receptor
FT superfamily member 18.
FT TOPO_DOM 26 162 Extracellular (Potential).
FT TRANSMEM 163 183 Potential.
FT TOPO_DOM 184 241 Cytoplasmic (Potential).
FT REPEAT 34 72 TNFR-Cys 1.
FT REPEAT 74 112 TNFR-Cys 2.
FT REPEAT 115 153 TNFR-Cys 3.
FT CARBOHYD 146 146 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 49 By similarity.
FT DISULFID 74 86 By similarity.
FT DISULFID 81 94 By similarity.
FT DISULFID 115 134 By similarity.
FT DISULFID 128 153 By similarity.
FT VARSPPLIC 135 241 By similarity.
FT TQGFLLTFFGNKTHNAVCPGSPPAEPLGMLTVLLAVAA
FT CVLLLSAQGLHILWLRSCMPRETQLLLEVPSPEDAR
FT SCFFPEERGERGAEEKRLGLDW -> CWRCKRRPKTPE
FT AASSPRKSGASDRQRSGGWETGCEPRGPPTAASPP
FT GAQQAALRSALGRALLPWQKRWGEGSDQRPCCSSAA
FT AAGFCRRERETQWPPSSLAGPDGVGS (in isoform
FT 2).
FT /FTID=VSP 006508.
FT SQCMWPRE -> K (in Ref. 2).
FT CONFLICT 194 201 90DC3B4AA7B82CBE CRC64;
FT SEQUENCE 241 AA; 26000 MW; 26000 MW; 90DC3B4AA7B82CBE CRC64;
Query Match 56.5%; Score 35; DB 1; Length 241;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 RLCRIWVIRVCR 12
Db 48 RCCRVTHTCCR 59
RESULT 81
Q5U014_HUMAN PRELIMINARY; PRT; 241 AA.
AC Q5U014;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 18.
GN Names=TNFRSF18; ORFNames=RP5-902P8.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
RT vector."
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Harrison E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT019531; AAY38338.1; -; mRNA.
DR EMBL; AL162741; CAI23247.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7B82CBE CRC64;

Query Match 56.5%; Score 35; DB 2; Length 241;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 RLCRIWVIRVCR 12
Db 48 RCCRVTHTCCR 59
RESULT 82
NFI_AERPE STANDARD; PRT; 255 AA.
AC Q9YESS;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endonuclease V (EC 3.1.21.7) (Deoxyinosine 3' endonuclease)
DE (Deoxyribonuclease V) (DNase V).
GN Name=nfi; OrderedLocusNames=APE0506;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -!- FUNCTION: Selectively cleaves double-stranded DNA at the second
CC phosphodiester bond 3' to a deoxyinosine leaving behind the intact
CC lesion on the nicked DNA. Acts in DNA repair (By similarity).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage at apurinic or
CC apyrimidinic sites to products with a 5'-phosphate.
CC -!- COFACTOR: Magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the endonuclease V family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; BA000002; BAA79471.1; ALT_INIT; Genomic_DNA.
DR PTR; C72747; C72747.
DR HAMAP; MF_00801; -; 1.
DR InterPro; IPR007581; Endonuc V.
DR Pfam; PF04493; Endonuclease_5; 1.
DR KW Complete proteome; DNA damage; DNA repair; Endonuclease; Hydrolase;
KW Magnesium; Nuclease.
SQ SEQUENCE 255 AA; 27258 MW; 2F84970A30351891 CRC64;
Query Match 56.5%; Score 35; DB 1; Length 255;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 CRIVWIRVC 11
Db 69 CRVVISRVC 77
RESULT 83
Q5T7K5_HUMAN PRELIMINARY; PRT; 255 AA.
ID Q5T7K5_HUMAN
AC Q5T7K5;

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DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 18.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Harrison B.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162741; CAI23246.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 255 AA; 26827 MW; C986652AC97AF2CC CRC64;

Query Match 56.5%; Score 35; DB 2; Length 255;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LCRVWVIRVC 12
Db 48 RCRVHTTRCC 59

RESULT 84
Q5SNS9 BRARE PRELIMINARY; PRT; 271 AA.
AC Q5SNS9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel potassium channel tetramerisation domain protein.
GN Name=OTDARP0000004599; ORFNames=CH211-192K9.2-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL954739; CAI11691.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR00210; BTF POZ.
DR InterPro; IPR003131; K_tetra.
DR Pfam; PF02214; K_tetra; 1.
DR SMART; SM00225; BTF; 1.
KW Ionic channel.
SQ SEQUENCE 271 AA; 30763 MW; C80EBA32303F61F5 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 271;
Best Local Similarity 60.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LCRVWVIRVC 10
Db 150 RMCCEVVRV 159

RESULT 85
Q5TTS3 ANOGA PRELIMINARY; PRT; 304 AA.
AC Q5TTS3;

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DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ENSANGP00000028647 (Fragment).
GN ORFNames=ENSANGG00000022428;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=PEST;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=PEST;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008859; EAL40916.1; -; Genomic DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR011611; Pfam; PF00294; PfkB; 1.
DR Pfam; PF00294; PfkB; 1.
FT NON TER 1 304
FT NON TER 304 304
SQ SEQUENCE 304 AA; 34033 MW; 146A225E32E54494 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 304;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRVWVIRVC 11
Db 11 LCNIDIIQVC 20

RESULT 86
Q6MPUS BDEBA PRELIMINARY; PRT; 320 AA.
AC Q6MPUS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE GDEF domain protein.
GN OrderedLucusNames=Bd0742;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RC PubMed=14752164; DOI=10.1126/science.1093027;
RX Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842648; CAE78699.1; -; Genomic DNA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR00160; GGDEF.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00990; GGDEF; 1.
DR SMART; SM00267; DUF1; 1.
DR SMART; SM00240; FHA; 1.
DR TIGRFAMs; TIGR00254; GGDEF; 1.
DR PROSITE; PS00006; FHA_DOMAIN; 1.

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DR PROSITE; PS50887; GGBDF; 1.
KW Complete proteome.
SQ SEQUENCE 320 AA; 34888 MW; 16F693750DD13330 CRC64;

Query Match
Best Local Similarity 56.5%; Score 35; DB 2; Length 320;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVIRVC 12
Db 218 LCRIVITKLIR 228
|||||:::|

RESULT 87
Q8A835_BACTN
ID Q8A835_BACTN PRELIMINARY; PRT; 368 AA.
AC Q8A835;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase.
GN OrderedLocusNames=BT1339;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
[1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=VPI-5482 / ATCC 29148;
RC MEDLINE=22550858; PubMed=126631928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RT Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016931; AA076446.1; -; Genomic_DNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR00715; Glyco trans 4.
DR InterPro; IPR003524; PNACPept trans.
DR Pfam; PF00953; Glycos transf 4; 1.
DR PROSITE; PS01348; MRAV_2; UNKNOWN_1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 368 AA; 41118 MW; 805CBBE9FE00D3C2 CRC64;

Query Match
Best Local Similarity 50.0%; Score 35; DB 2; Length 368;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 RIVVIRVC 11
Db 279 RVVIVRIC 286
|||||:::|

RESULT 88
Q8YRF6_ANASP
ID Q8YRF6_ANASP PRELIMINARY; PRT; 414 AA.
AC Q8YRF6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alr3492 protein.
GN OrderedLocusNames=alr3492;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
[1]
NUCLEOTIDE SEQUENCE.
RP MEDLINE=21595285; PubMed=11759840;
RX Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Iehikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; BA000019; BAB75191.1; -; Genomic_DNA.
DR PIR; AE2242; AE2242.
KW Complete proteome.
SQ SEQUENCE 414 AA; 47601 MW; E415AE3249B9D324 CRC64;

Query Match
Best Local Similarity 45.5%; Score 35; DB 2; Length 414;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RLCRIVIRVC 11
Db 82 RLCRLWVRPC 92
|||||:::|

RESULT 89
Q4S8L3_TETNG
ID Q4S8L3_TETNG PRELIMINARY; PRT; 441 AA.
AC Q4S8L3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAF14705, whole genome shotgun sequence.
GN ORFNames=GSTENG00022288001;
OS Tetraodon nigroviridis (Green puffer).
OC Tetraodon nigroviridis; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei; Neoteleostei;
OC Actinopterygii; Neopterygii; Teleostei; Tetraodontiformes;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
[1]
NUCLEOTIDE SEQUENCE.
RP Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
RA Maucud E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lindblad-Toh K., Birren B., Birren B., Saurin W., Scarpelli C.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]
NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the AdoMet synthetase family.
DR EMBL; CAE01014705; CAG03019.1; -; Genomic_DNA.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF02773; S-AdoMet_synth_C; 1.
DR Pfam; PF00438; S-AdoMet_synth_N; 1.
DR PIRSF; PIRSF000497; MAT; 1.
DR TIGRFAMs; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.

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KW ATP-binding; Magnesium; Metal-binding; Nucleotide-binding;
 KW One-carbon metabolism; Potassium; Transposase;
 SQ SEQUENCE 441 AA; 48551 MW; 98452C1A1ECB45E3 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 441;
 Best Local Similarity 58.3%; Pred. No. 6.2e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
 ||||| :|||
 Db 308 RLCRRVLQVQR 319

RESULT 90

ID Q7XQNO_ORYSA PRELIMINARY; PRT; 466 AA.
 AC Q7XQNO;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE OSJNB0089K21.6 protein.
 GN Name=OSJNB0089K21.6;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=12447439; DOI=10.1038/nature01183;
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 DR EMBL; AL606441; CAE03052.2; -; Genomic_DNA.
 DR Gramene; Q7XQNO;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
 DR GO; GO:0006865; P:amino acid transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002422; AA/rel_permease2.
 DR Pfam; PF01490; Aa trans; I.
 SQ SEQUENCE 466 AA; 50746 MW; B49F6F008C387F54 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 466;
 Best Local Similarity 55.6%; Pred. No. 6.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
 ||| :|||
 Db 371 CRVNLVRC 379

RESULT 91

ID Q4UFC4_THEAN PRELIMINARY; PRT; 470 AA.
 AC Q4UFC4;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=TA15145;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;

OC Theileria.
 OX NCBI_TaxID=5874;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ankara isolate clone C9;
 RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
 RA Hall N., Barrell B.G.;
 RT "The chromosome 2 sequence of Theileria annulata.";
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR940348; CAI74192.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 55436 MW; 8EFD334788BDC3CE CRC64;

Query Match 56.5%; Score 35; DB 2; Length 470;
 Best Local Similarity 33.3%; Pred. No. 6.6e+02;
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
 ||| :|||
 Db 234 RVCVMSMKICR 245

RESULT 92

ID Q9BU21_HUMAN PRELIMINARY; PRT; 477 AA.
 AC Q9BU21;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE C9orf86 protein.
 GN Name=C9orf86;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
 DR EMBL; BC002945; AA02945-2; -; mRNA.
 DR GO; GO:0005525; P:GTP binding; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro; IPR003579; GTPase Rab.
 DR InterPro; IPR001806; Ras trnsfrmg.
 DR PRINTS; PR00449; RASTRNSFRMG.

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DR SMART: SM00175; RAB; 1.
SQ SEQUENCE 477 AA; 52679 MW; ABF586658421D4E CRC64;

Query Match 56.5%; Score 35; DB 2; Length 477;
Best Local Similarity 63.6%; Pred. No. 6.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIIVIRVC 11
DB 356 RLCRCFPAVVC 366

RESULT 93
Q9JTF0_NEIMA PRELIMINARY; PRT; 505 AA.
AC Q9JTF0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative two component sensor kinase.
GN OrderedLocustNames=NMA1803;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RA "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162757; CAB85029.1; -; Genomic_DNA.
DR PIR; A81806; A81806.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kin_N.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HisKA; 1.
DR SMART; SM00388; HisKA; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
KW Complete proteome; Kinase.
SQ SEQUENCE 505 AA; 56509 MW; 6CAAF8758E7AB186 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 505;
Best Local Similarity 50.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIIVIRVC 12
DB 353 KLCKIIDGNVC 364

RESULT 94
Q6Z4L0_ORYSA PRELIMINARY; PRT; 507 AA.
AC Q6Z4L0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative UDP-glucosyltransferase.

```

```

GN Name=OSJNBa0081K20.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
RT clone:OSJNBa0081K20.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the UDP-glucosyltransferase family.
EMBL; AF005171; BAC83830.1; -; Genomic_DNA.
DR Gramene; Q6Z4L0; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; UNKNOWN_1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 507 AA; 55460 MW; C569177153540D0F CRC64;

Query Match 56.5%; Score 35; DB 2; Length 507;
Best Local Similarity 44.4%; Pred. No. 7.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVIVRVC 11
DB 252 CRLIIVRTC 260

RESULT 95
Q5T5R6_HUMAN PRELIMINARY; PRT; 520 AA.
AC Q5T5R6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE OTTHUMP00000022610.
GN Name=RP11-216L13.9; ORFNames=RP11-216L13.9-005;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Brown A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
EMBL; AL355987; CA112686.1; -; Genomic_DNA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR003579; GTPase_Rab.
DR InterPro; IPR001806; Ras_trnsfrmg.
DR PRINTS; PR00449; RASTRNSFRMG.
DR SMART; SM00175; RAB; 1.
SQ SEQUENCE 520 AA; 57397 MW; ABB2BD2287F358BF CRC64;

Query Match 56.5%; Score 35; DB 2; Length 520;
Best Local Similarity 63.6%; Pred. No. 7.3e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIIVIRVC 11
DB 399 RLCRCFPAVVC 409

RESULT 96
Q4SYE4_TETNG PRELIMINARY; PRT; 556 AA.
ID Q4SYE4_TETNG

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Q45YE4;
 13-SEP-2005 (TrEMBLrel. 31, Created)
 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 Chromosome 5 SCAR12081, whole genome shotgun sequence.
 ORFNames=GSTENG00010371001;
 Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraontoidea; Tetraodontidae; tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA David V., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn W., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; CAAB01012081; CAF94338.1; -; Genomic_DNA.
 DR InterPro; IPR002293; AA/re_l_permease1.
 DR InterPro; IPR004841; Permease_region.
 DR Pfam; PF00324; AA/permease; 1.
 KW Transmembrane; Transport.
 SQ SEQUENCE 556 AA; 60368 MW; FA8B07381C684BCB CRC64;
 Query Match 56.5%; Score 35; DB 2; Length 556;
 Best Local Similarity 50.0%; Pred. No. 7.7e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RLCLRVIRVCR 12
 Db 379 RLCTGVLLRSQ 390
 |||||:::
 PRT; 573 AA.
 RESULT 97
 Q4K623 PSEF5
 ID O4K623 PSEF5 PRELIMINARY; PRT; 573 AA.
 AC O4K623;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE DnaJ domain protein, putative.
 GN ORFNames=PFL_5233;
 OS Pseudomonas fluorescens (strain Pf-5).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=220664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Pf-5;
 RX PubMed=15980861; DOI=10.1038/nbt1110;
 RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
 RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
 RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
 RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,

RA Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;
 RT "Complete genome sequence of the plant commensal Pseudomonas
 fluorescens Pf-5.";
 RL Nat. Biotechnol. 23:873-878(2005).
 DR EMBL; CP000076; AA/94452.1; -; Genomic_DNA.
 SQ SEQUENCE 573 AA; 65544 MW; PFE82A26240A35E0 CRC64;
 Query Match 56.5%; Score 35; DB 2; Length 573;
 Best Local Similarity 87.5%; Pred. No. 7.9e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 IIVIRVCR 12
 Db 552 IIVIRVCR 559
 |||||:
 PRT; 593 AA.
 RESULT 98
 Q8BHX6 MOUSE
 ID Q8BHX6 MOUSE PRELIMINARY; PRT; 593 AA.
 AC Q8BHX6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
 library, clone:4632413L16 product:similar to HYPOTHETICAL 84.9 kDa
 DE PROTEIN DKFZP564C186.
 GN Name=AF155546;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RC The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=SKIN;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes";
RN Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=SKIN;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=SKIN;
RX STRAIN=C57BL/6J; TISSUE=SKIN;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK076287; BAC36289.1; -, mRNA.
DR MGI; MGI:1931051; AF155546.
DR InterPro; IPR005343; UPF0120.
DR Pfam; PF03715; UPF0120; 1.
KW Hypothetical protein.
SQ SEQUENCE 593 AA; 68267 MW; A3528A22AACABFCD CRC64;

Query Match 56.5%; Score 35; DB 2; Length 593;
Best Local Similarity 63.6%; Pred. No. 8.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVIRVCR 12
| :|:|:|:|
DB 159 LAFVLIRVCR 169

RESULT 99
Q4RUV6 TETNG

ID Q4RUV6_TETNG PRELIMINARY; PRT; 598 AA.

AC Q4RUV6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 12 SCAF14993, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG00028589001;
GN Tetraodon nigroviridis (Green puffer).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR ENBL; CAAE01014993; CAG07796.1; -; Genomic_DNA.
FT NON TER 598
SQ SEQUENCE 598 AA; 66715 MW; 2C5C5099FC4260E8 CRC64;
Query Match 56.5%; Score 35; DB 2; Length 598;
Best Local Similarity 54.5%; Pred. No. 8.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LCRIVIRVCR 11
| :|:|:|:|
DB 205 RVCVCVCRVC 215

RESULT 100
Q4SM47 TETNG
ID Q4SM47_TETNG PRELIMINARY; PRT; 687 AA.
AC Q4SM47;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 13 SCAF14555, whole genome shotgun sequence.
DE ORFNames=GSTENG00015937001;
GN Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR ENBL; CAAE01014555; CAF98285.1; -; Genomic_DNA.
SQ SEQUENCE 687 AA; 77882 MW; BBE3D218CC2AB3C4 CRC64;

Query Match 56.5%; Score 35; DB 2; Length 687;
Best Local Similarity 63.6%; Pred. No. 9.4e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 12
||| ||
Db 94 LCRFVVCQCR 104

Search completed: February 15, 2006, 11:10:17
Job time : 244 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 11:04:36 ; Search time 80 Seconds

(without alignments)
65.907 Million cell updates/sec

Title: US-10-657-851-37

Perfect score: 62

Sequence: 1 RLCRIVIRVCR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	12	2 AAW66398	Aaw66398 Cationic
2	62	100.0	12	3 AAY91697	Aay91697 Cationic
3	62	100.0	12	3 AAY55057	Aay55057 Non-amida
4	62	100.0	12	3 AAY67330	Aay67330 Wild type
5	62	100.0	12	3 AAY67346	Aay67346 Antimicro
6	62	100.0	12	4 AAB91846	Aab91846 Antimicro
7	62	100.0	12	4 AAB91855	Aab91855 Antimicro
8	62	100.0	12	5 ABB07700	Abb07700 Bovine li
9	62	100.0	12	5 AAU91001	Aau91001 Transplan
10	62	100.0	12	5 ABB81256	Abb81256 Bacteneci
11	62	100.0	12	5 ABB81257	Abb81257 Linear Ba
12	62	100.0	12	5 AAO15562	Aao15562 Bovine li
13	62	100.0	12	6 ABB05974	Abb05974 Cationic
14	62	100.0	12	6 AAB34432	Aab34432 Cow bacte
15	62	100.0	12	8 AAD35346	Aad35346 Antimicro
16	62	100.0	12	8 ADQ14302	Adq14302 Peptide u
17	62	100.0	12	9 ADX08379	Adx08379 BNP-1 ant
18	62	100.0	12	9 ADY67437	Ady67437 Tumor cel
19	62	100.0	14	3 AAY67340	Aay67340 Antimicro
20	62	100.0	18	3 AAY67347	Aay67347 Antimicro
21	62	100.0	155	5 ABB07704	Abb07704 Bovine pe
22	62	100.0	155	5 AAU90993	Aau90993 Transplan
23	62	100.0	155	9 ADX08371	Adx08371 Bacteneci
24	56	90.3	12	8 ADR82249	Adr82249 Cell perm

25	56	90.3	12	8 ADT61094	Adt61094 Novel int
26	56	90.3	12	8 ADT86670	Adt86670 Bacteneci
27	56	90.3	12	8 ADU67508	Adu67508 Bacteneci
28	56	90.3	12	8 ADU26587	Adu26587 Cell perm
29	56	90.3	12	9 ADW25979	Adw25979 Bacteneci
30	52	83.9	12	3 AAY67332	Aay67332 Antimicro
31	51.5	83.1	13	3 AAY67341	Aay67341 Antimicro
32	51.5	83.1	13	3 AAY67342	Aay67342 Antimicro
33	51.5	83.1	15	3 AAY67343	Aay67343 Antimicro
34	49	79.0	12	3 AAY67334	Aay67334 Antimicro
35	49	79.0	14	3 AAY67338	Aay67338 Antimicro
36	47.5	76.6	11	6 ABB71542	Abb71542 Bovine ne
37	45	72.6	12	3 AAY67335	Aay67335 Antimicro
38	44	71.0	12	3 AAY91867	Aay91867 Amino aci
39	44	71.0	12	3 AAY67331	Aay67331 Antimicro
40	44	71.0	12	6 ADA00619	Ada00619 Antimicro
41	44	71.0	12	6 ABR63789	Abr63789 Bovine ca
42	44	71.0	12	7 ADC98988	Adc98988 Synthetic
43	44	71.0	12	9 ADY79756	Ady79756 Amino aci
44	43	69.4	12	3 AAY67337	Aay67337 Antimicro
45	42	67.7	12	3 AAY67333	Aay67333 Antimicro
46	42	67.7	12	5 ABB81258	Abb81258 Bac2S ant
47	42	67.7	304	3 AAG25236	Aag25236 Arabidops
48	42	67.7	618	3 AAG46462	Aag46462 Arabidops
49	42	67.7	662	3 AAG46480	Aag46480 Arabidops
50	42	67.7	662	7 ADE25067	Ade25067 Plant gro
51	41	66.1	12	3 AAY67336	Aay67336 Antimicro
52	41	66.1	131	4 ADM19746	Adm19746 Protein e
53	40.5	65.3	14	3 AAY67339	Aay67339 Antimicro
54	39	62.9	447	7 ABB88679	Abb88679 Rice abio
55	38.5	62.1	13	3 AAY67344	Aay67344 Antimicro
56	38	61.3	50	6 ABO14090	Abol14090 Novel hum
57	38	61.3	50	8 ADN60787	Adn60787 Human sec
58	38	61.3	51	2 AAY27685	Aay27685 Human sec
59	38	61.3	51	8 ADG78496	Adg78496 Human sec
60	38	61.3	58	4 AAU65577	Aau65577 Propionib
61	38	61.3	58	6 ABB62096	Abb62096 Propionib
62	38	61.3	71	4 AAU45256	Aau45256 Propionib
63	38	61.3	71	6 ABA41775	Abm41775 Propionib
64	38	61.3	343	8 ADM98644	Adm98644 Geranylge
65	38	61.3	343	8 ADM98612	Adm98612 Geranylge
66	37	59.7	60	4 AAU58705	Aau58705 Propionib
67	37	59.7	60	6 ABB55224	Abb55224 Propionib
68	37	59.7	181	7 ABO81457	Abol1457 Pseudomon
69	37	59.7	378	4 ABB64054	Abb64054 Drosophill
70	37	59.7	1618	4 ABB59829	Abb59829 Protein #
71	37	59.7	1953	6 AAE35490	Aae35490 Streptomy
72	36	58.1	26	7 ADE09150	Ade09150 Novel pro
73	36	58.1	47	4 AAU14414	Aau14414 Human nov
74	36	58.1	47	4 AAU14178	Aau14178 Human nov
75	36	58.1	47	8 ADH80732	Adh80732 Human pol
76	36	58.1	65	4 AAU47375	Aau47375 Propionib
77	36	58.1	65	6 ABB43894	Abb43894 Propionib
78	36	58.1	75	4 ABB66840	Abb66840 Drosophill
79	36	58.1	75	8 ABO55476	Abol55476 Human gen
80	36	58.1	115	4 ABB14129	Abb14129 Novel hum
81	36	58.1	269	7 ADC87319	Adc87319 Human GPC
82	36	58.1	284	8 ADX68272	Adx68272 Plant ful
83	36	58.1	334	7 ADC95320	Adc95320 E. faeciu
84	36	58.1	391	8 ADS43623	Ads43623 Bacterial
85	36	58.1	462	7 ADK41695	Adk41695 Maize ani
86	36	58.1	471	8 ADT58108	Adt58108 Plant pol
87	36	58.1	517	8 ADX68104	Adx68104 Plant ful
88	36	58.1	537	8 ADJ48834	Adj48834 Oil-assoc
89	36	58.1	645	8 ADM40441	Adm40441 Plant pol
90	36	58.1	709	8 ADM48165	Adm48165 Polypepti
91	36	58.1	762	4 ABB58525	Abb58525 Drosophill
92	36	58.1	861	9 ABB58367	Abb58367 Ancestral
93	36	58.1	861	9 ADW38369	Adw38369 Ancestral
94	36	58.1	861	9 ADW38365	Adw38365 Ancestral
95	36	58.1	913	4 AAM41078	Aam41078 Human pol
96	36	58.1	913	8 ADS12128	Ads12128 Human the
97	35	56.5	123	7 ABB85214	Abb85214 Mouse pro

98 35 56.5 190 7 ABM89108 Abm89108 Rice abio
 99 35 56.5 208 4 ABG16152 ABG16152 Novel hum
 100 35 56.5 228 2 AAW37840 Aaw37840 Truncated

ALIGNMENTS

RESULT 1
 AAW66398
 ID AAW66398 standard; peptide; 12 AA.
 AC
 XX AAW66398;
 XX
 DT 12-JAN-1999 (first entry)
 XX
 DE Cationic peptide bactenecin.
 XX
 KW Indolicidin analogue; resistance; cationic peptide; antibiotic;
 KW bacterial infection; tolerance; antibacterial; microorganism; bacteria;
 KW fungus; parasite; virus.
 XX
 OS Bos taurus.
 XX
 PN WO9840401-A2.
 XX
 PD 17-SEP-1998.
 XX
 PF 10-MAR-1998; 98WO-CA000190.
 XX
 PR 10-MAR-1997; 97US-0040649P.
 PR 20-AUG-1997; 97US-00915314.
 PR 26-SEP-1997; 97US-0060099P.
 PR 25-FEB-1998; 98US-00030619.
 XX
 PA (MICR-) MICROLOGIX BIOTECH INC.
 XX
 PI Fraser JR, West MHP, Mcnicol PJ;
 XX
 DR WPI; 1998-520800/44.
 XX
 XX New indolicidin peptide analogues - useful for, e.g. enhancing activity
 PT of antibiotic or overcoming tolerance, acquired resistance or inherent
 PT resistance of microorganisms.
 XX
 PS Disclosure; Page 7; 105pp; English.

XX AAW66393 to AAW66469 represent native cationic peptides from the present
 CC invention. The present invention describes compositions and methods for
 CC treating infection, especially bacterial infections. The compositions and
 CC methods use cationic peptides in combination with an antibiotic agent
 CC which are then administered to a patient to enhance the activity of the
 CC antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance;
 CC and (c) inherent resistance. The combinations of antibiotics and cationic
 CC peptides can provide synergistic activity against a microorganism that is
 CC tolerant, inherently resistant, or has acquired resistance to an
 CC antibiotic agent. They can be used for killing e.g. bacteria, fungi,
 CC parasites and viruses
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RLCRIWVIRVCR 12
 Db 1 RLCRIWVIRVCR 12
 RESULT 2
 AAY91697
 ID AAY91697 standard; peptide; 12 AA.

Query Match 100.0%; Score 62; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RLCRIWVIRVCR 12
 Db 1 RLCRIWVIRVCR 12

RESULT 2
 AAY91697
 ID AAY91697 standard; peptide; 12 AA.

XX AAY91697;
 AC
 XX 06-JUN-2000 (first entry)
 DT
 DE Cationic peptide Bactenecin amino acid sequence.
 XX
 KW Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;
 KW leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma;
 KW breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
 KW multidrug resistance.
 XX
 OS Unidentified.
 XX
 PN WO9965506-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 14-JUN-1999; 99WO-CA000552.
 XX
 PR 12-JUN-1998; 98US-00096541.
 XX
 PA (MICR-) MICROLOGIX BIOTECH INC.
 XX
 PI Friedland HD, Krieger TJ, Taylor R, Erfle D, Fraser JR, West MHP;
 XX
 DR WPI; 2000-223549/19.
 XX
 PF Novel pharmaceutical composition containing optionally activated
 PT polyoxyalkylene-modified cationic peptides, useful for treating tumors.
 XX
 PS Disclosure; Page 8; 94pp; English.
 XX
 CC This sequence represents a cationic peptide amino acid sequence, which
 CC can be used in the pharmaceutical composition of the invention. The
 CC invention relates to a pharmaceutical composition containing at least one
 CC activated polyoxyalkylene (APO)-modified cationic peptide. The
 CC modification of peptides with APO increases their activity against tumour
 CC cells, including those with a multidrug resistant phenotype. The
 CC pharmaceutical composition can be used to treat tumours, specifically
 CC lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary,
 CC cervix, uterus, skin, prostate, liver and colon
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 62; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RLCRIWVIRVCR 12
 Db 1 RLCRIWVIRVCR 12
 RESULT 3
 AAY55057
 ID AAY55057 standard; peptide; 12 AA.
 XX
 AC AAY55057;
 XX
 DT 23-FEB-2000 (first entry)
 XX
 DE Non-amidated bactenecin peptide.
 XX
 KW Indolicidin; bactenecin; sulphate-reducing bacteria; growth inhibitor;
 KW corrosion; degradation; metal; concrete; cement; dental implant; biofilm.
 XX
 OS Bacillus sp.
 XX
 PN WO9956553-A1.
 XX
 PD 11-NOV-1999.
 XX

CC AAY67330-Y67347) derived from bactenecin, and includes analogues,
 CC derivatives, amidated variations and conservative variation. The peptides
 CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
 CC antifungal activities. The antimicrobial peptides are useful for
 CC inhibiting the growth of bacteria including both gram positive and
 CC negative species including Escherichia coli, Pseudomonas aeruginosa and
 CC Salmonella typhimurium. The peptides can be used to inhibit endotoxaemia
 CC or sepsis associated disorders, such as septic shock. The peptides can
 CC also be used to inhibit the growth of a eukaryotic cell, especially an
 CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
 CC can also be used to inhibit a cell proliferation-associated disorder
 XX
 SQ

Sequence 12 AA;

Query Match 100.0%; Score 62; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIWVIRVCR 12
 DB 1 RLCRIWVIRVCR 12
 |||||

RESULT 6
 AAB91846
 ID AAB91846 standard; peptide; 12 AA.
 XX
 AC AAB91846;
 XX
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Antimicrobial peptide SEQ ID NO:1022.
 XX
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200069900-A2.
 PN
 PR 23-NOV-2000.
 PD
 XX
 XX 17-MAY-2000; 2000WO-US013576.
 PF
 XX
 XX 17-MAY-1999; 99US-0134406P.
 PR
 PR 10-SEP-1999; 99US-0153406P.
 PR
 PR 15-OCT-1999; 99US-0159783P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 PA
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 PI
 XX WPI; 2001-112059/12.
 DR
 XX

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 XX Disclosure; Page 530; 733pp; English.
 PS
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIWVIRVCR 12
 DB 1 RLCRIWVIRVCR 12
 |||||

RESULT 7
 AAB91855
 ID AAB91855 standard; peptide; 12 AA.
 XX
 AC AAB91855;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Antimicrobial peptide SEQ ID NO:1031.
 XX
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200069900-A2.
 PN
 PR 23-NOV-2000.
 PD
 XX
 XX 17-MAY-2000; 2000WO-US013576.
 PF
 XX
 XX 17-MAY-1999; 99US-0134406P.
 PR
 PR 10-SEP-1999; 99US-0153406P.
 PR
 PR 15-OCT-1999; 99US-0159783P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 PA
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 PI
 XX WPI; 2001-112059/12.
 DR
 XX

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 XX Disclosure; Page 533; 733pp; English.
 PS
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 12 AA;

XX

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SQ Sequence 12 AA;
  Query Match      100.0%; Score 62; DB 4; Length 12;
  Best Local Similarity 100.0%; Pred. No. 0.0028;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLCRIWVIRVCR 12
Db 1 RLCRIWVIRVCR 12
  |||||
  |||||

RESULT 8
ABB07700
ID ABB07700 standard; peptide; 12 AA.
XX
AC ABB07700;
XX
DT 10-JUN-2002 (first entry)
XX
DE Bovine linear or cyclised antimicrobial dodecapeptide.
XX
KW Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
KW antigen presenting cell; adjuvant; bovine; indolicidin.
XX
OS Synthetic.
OS Bos sp.
XX
PN WO200213857-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-EP009529.
XX
PR 17-AUG-2000; 2000AT-00001416.
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
XX
WPI; 2002-269154/31.
XX
Vaccine for active immunization or for preparing an adjuvant for
PT enhancing an immune response to at least one antigen, comprises at least
PT one antigen and at least one cathelicidin derived antimicrobial peptide.
XX
PS Claim 10; Page 57; 65pp; English.
XX
The invention relates to a vaccine comprising at least one antigen and at
CC least one cathelicidin derived antimicrobial peptide or its derivative.
CC The vaccine is useful for active immunization, especially of humans or
CC animals without protection against the specific antigen. The cathelicidin
CC derived antimicrobial peptide is useful in the preparation of an adjuvant
CC for enhancing the immune response to at least one antigen, where the
CC adjuvant enhances the uptake of at least one antigen in antigen
CC presenting cells (APC), and the adjuvant is added to the vaccine. The
CC present sequence represents a bovine derived linear or cyclised
CC antimicrobial dodecapeptide, used in the vaccine
XX
SQ Sequence 12 AA;
  Query Match      100.0%; Score 62; DB 5; Length 12;
  Best Local Similarity 100.0%; Pred. No. 0.0028;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLCRIWVIRVCR 12
Db 1 RLCRIWVIRVCR 12
  |||||
  |||||

RESULT 9
AAU91001
ID AAU91001 standard; peptide; 12 AA.
XX

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AC AAU91001;
XX
DT 05-JUN-2002 (first entry)
XX
DE Transplant media associated defensin peptide #2.
XX
KW Transplant; antimicrobial peptide; pore forming agent;
KW cell surface receptor binding compound; kidney transplant; cardioplegia;
KW organ transplant; transplant rejection; defensin.
XX
OS Bos taurus.
XX
PN WO200209738-A1.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-US023785.
XX
PR 28-JUL-2000; 2000US-0221632P.
PR 17-NOV-2000; 2000US-0249602P.
PR 15-MAY-2001; 2001US-0290932P.
XX
PA (MURP/) MURPHY C J.
XX
PI Murphy CJ, Reid TW, Mcanulty JF;
XX
WPI; 2002-268995/31.
XX
Media comprising antimicrobial polypeptides or pore forming agents and/or
PT cell surface receptor binding compounds useful for the storage and
PT preservation of organs prior to transplant.
XX
PS Claim 8; Page 27; 78pp; English.
XX
The invention describes new transplant compositions comprising
CC antimicrobial polypeptides or pore forming agents and/or cell surface
CC receptor binding compounds. The media is capable of extending the
CC preservation period past 72 hours and can provide organs with increased
CC functionality upon transplant. Animals receiving kidneys stored in the
CC media of the present invention for either three or four days had serum
CC creatinine levels of less than half of those observed in control animals
CC receiving kidneys stored in UW solution (defined in the specification)
CC alone. Lower serum creatinine levels are indicative of healthier kidneys
CC and a more preferable prognosis for the transplant patient. The media of
CC the invention are useful for decreasing the incidence and/or severity of
CC delayed graft function in patients receiving transplanted kidneys stored
CC and/or treated in the media. The media may also be used in procedures
CC such as cardioplegia. It is contemplated that transplant of healthier
CC organs leads to a decrease in chronic rejection. This sequence represents
CC an antimicrobial defensin peptide studied in the development of the
CC transplant media
XX
SQ Sequence 12 AA;
  Query Match      100.0%; Score 62; DB 5; Length 12;
  Best Local Similarity 100.0%; Pred. No. 0.0028;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLCRIWVIRVCR 12
Db 1 RLCRIWVIRVCR 12
  |||||
  |||||

RESULT 10
ABB81256
ID ABB81256 standard; peptide; 12 AA.
XX
AC ABB81256;
XX
DT 20-AUG-2002 (first entry)
XX
DE Bactenecin antibacterial peptide SEQ ID NO:23.
XX

```

KW Antibacterial; glycopeptide; peptidic membrane associating element;
 KW bacterial infection; vancomycin; peptidoglycan biosynthesis inhibition;
 KW antibiotic.

OS Synthetic.

PH Key Location/Qualifiers
 FT Disulfide-bond 3. 11

XX WO200236612-A1.

XX 10-MAY-2002.

XX 02-NOV-2001; 2001WO-GB004867.

XX 03-NOV-2000; 2000GB-00026924.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX (ADPR-) ADPROTECH LTD.

XX Cooper MA, Betley JR;

XX WPI; 2002-471498/50.

XX Antibacterial compound, useful for the treatment of a bacterial infection
 PT by e.g. gram positive or negative bacteria, comprises a conjugate of
 PT glycopeptide and peptidic membrane-associating element.

XX Disclosure; Page 21; 64pp; English.

XX The present invention describes an antibacterial compound (I), comprising
 CC a conjugates of glycopeptide and peptidic membrane-associating elements.
 CC (I) comprises the formula V-L-W-X, where: V = a glycopeptide moiety that
 CC inhibits peptidoglycan biosynthesis in bacteria; L = a linking group; W =
 CC a peptidic membrane-associating element; and X = H or a membrane-
 CC insertive element. Also described: (1) a method of treating or preventing
 CC a bacterial infection, comprising the administration of (I); and (2) use
 CC of (I) in the manufacture of a medicament for the treatment or prevention
 CC of a bacterial infection. (I) are used in the manufacture of a medicament
 CC for the treatment or prophylaxis of a bacterial infection in a human or
 CC animal body, including both the gram positive and gram negative bacteria
 CC including Mycobacterium sp., Enterococcus sp., Escherichia sp.,
 CC Staphylococcus sp., Vibrio sp., Neisseria sp., Borrelia sp., Klebsiella
 CC sp., Hemophilus sp., Clostridium sp., Pseudomonas sp., Actinomyces sp.,
 CC Pneumococcus sp. or Salmonella sp., particularly antibiotic resistant
 CC bacterial strains. (I) are also useful as wound treatment agents to
 CC prevent adhesion of bacteria to matrix proteins, especially fibronectin,
 CC exposed in wound tissue; and for prophylactic use in dental treatment as
 CC an alternative to, or in conjunction with, antibiotic prophylaxis. (I)
 CC has stronger binding to bacterial membranes which have a higher
 CC proportion of acidic phospholipids than the eukaryotic organisms, also
 CC having a higher proportion of membrane associated biosynthetic proteins.
 CC Vancomycin shows an enhanced antimicrobial activity upon derivatisation
 CC with (I) and is effective to treat the antibiotic resistant bacterial
 CC strains. ABB81234 to ABB81272 represent peptides given in the
 CC exemplification of the present invention

XX Sequence 12 AA;

Query Match 100.0%; Score 62; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12

Db 1 RLCRIWVIRVCR 12

RESULT 11

ID ABB81257
 XX ABB81257 standard; peptide; 12 AA.

XX ABB81257;

XX 20-AUG-2002 (first entry)
 XX Linear Bac antibacterial peptide SEQ ID NO:24.

XX Antibacterial; glycopeptide; peptidic membrane associating element;
 KW bacterial infection; vancomycin; peptidoglycan biosynthesis inhibition;
 KW antibiotic.

OS Synthetic.

XX WO200236612-A1.

XX 10-MAY-2002.

XX 02-NOV-2001; 2001WO-GB004867.

XX 03-NOV-2000; 2000GB-00026924.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX (ADPR-) ADPROTECH LTD.

XX Cooper MA, Betley JR;

XX WPI; 2002-471498/50.

XX Antibacterial compound, useful for the treatment of a bacterial infection
 PT by e.g. gram positive or negative bacteria, comprises a conjugate of
 PT glycopeptide and peptidic membrane-associating element.
 XX Disclosure; Page 21; 64pp; English.

XX The present invention describes an antibacterial compound (I), comprising
 CC a conjugates of glycopeptide and peptidic membrane-associating elements.
 CC (I) comprises the formula V-L-W-X, where: V = a glycopeptide moiety that
 CC inhibits peptidoglycan biosynthesis in bacteria; L = a linking group; W =
 CC a peptidic membrane-associating element; and X = H or a membrane-
 CC insertive element. Also described: (1) a method of treating or preventing
 CC a bacterial infection, comprising the administration of (I); and (2) use
 CC of (I) in the manufacture of a medicament for the treatment or prevention
 CC of a bacterial infection. (I) are used in the manufacture of a medicament
 CC for the treatment or prophylaxis of a bacterial infection in a human or
 CC animal body, including both the gram positive and gram negative bacteria
 CC including Mycobacterium sp., Enterococcus sp., Escherichia sp.,
 CC Staphylococcus sp., Vibrio sp., Neisseria sp., Borrelia sp., Klebsiella
 CC sp., Hemophilus sp., Clostridium sp., Pseudomonas sp., Actinomyces sp.,
 CC Pneumococcus sp. or Salmonella sp., particularly antibiotic resistant
 CC bacterial strains. (I) are also useful as wound treatment agents to
 CC prevent adhesion of bacteria to matrix proteins, especially fibronectin,
 CC exposed in wound tissue; and for prophylactic use in dental treatment as
 CC an alternative to, or in conjunction with, antibiotic prophylaxis. (I)
 CC has stronger binding to bacterial membranes which have a higher
 CC proportion of acidic phospholipids than the eukaryotic organisms, also
 CC having a higher proportion of membrane associated biosynthetic proteins.
 CC Vancomycin shows an enhanced antimicrobial activity upon derivatisation
 CC with (I) and is effective to treat the antibiotic resistant bacterial
 CC strains. ABB81234 to ABB81272 represent peptides given in the
 CC exemplification of the present invention

XX Sequence 12 AA;

Query Match 100.0%; Score 62; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12

Db 1 RLCRIWVIRVCR 12

RESULT 12

ID AAO15562
 ID AAO15562 standard; protein; 12 AA.

XX AAO15562;
 AC 24-OCT-2002 (first entry)
 DT XX
 DE Bovine linear dodecapeptide.
 XX
 XX Anti-microbial peptide; antigenic peptide TRANSload; infection; tumour;
 KW antigen presenting cell; vaccine; carrier peptide; bovine; cow;
 KW linear dodecapeptide.
 XX
 XX Bos taurus.
 OS WO200232451-A1.
 XX
 XX 25-APR-2002.
 PD
 XX 18-OCT-2001; 2001WO-EP012041.
 PF
 XX 18-OCT-2000; 2000AT-00001789.
 XX
 XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 PA
 XX Fritz J, Mattner F, Zauner W, Nagy E, Buschle M;
 PI WPI; 2002-489874/52.
 XX
 XX Novel vaccine comprising an antigen and an immunostimulating substance
 PT that strongly enhances immune response to the co-administered antigen,
 PT and efficiently TRANSloads antigenic peptides into antigen presenting
 PT cells.
 XX
 XX Example 1; Page 32; 40pp; English.
 PS
 XX The invention comprises a vaccine that contains at least one antigen and
 CC a carrier peptide that is able to strongly enhance the immune response to
 CC the specific co-administered antigen. The carrier peptides of the
 CC invention are able to strongly enhance the immune response to a specific
 CC co-administered antigen and therefore constitutes a highly effective
 CC antigen. The carrier peptides efficiently TRANSload antigenic peptides
 CC into antigen presenting cells. The vaccine of the invention is useful for
 CC vaccinating a mammal against a specific antigen or group of specific
 CC antigens derived from: a virus (e.g. HIV or Epstein-Barr virus); bacteria
 CC ; fungi; parasites; or antigens from a tumour. The present amino acid
 CC sequence represents the bovine linear dodecapeptide which was used as a
 CC carrier peptide in an example of the invention
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 62; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RLCRIWIRVCR 12
 Db 1 RLCRIWIRVCR 12
 RESULT 13
 ABU59574
 ID ABU59574 standard; peptide; 12 AA.
 XX
 AC ABU59574;
 XX
 XX 22-APR-2003 (first entry)
 DT
 XX Cationic cancer -targeting peptide #6.
 DE
 XX Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;
 KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;
 KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;
 KW tumour; cationic cancer-targeting peptide.
 XX

OS Synthetic.
 XX
 PN US2002041898-A1.
 XX
 PD 11-APR-2002.
 XX
 XX 25-JUL-2001; 2001US-00912609.
 PF
 XX 05-JAN-2000; 2000US-00478124.
 PR
 PR 31-OCT-2000; 2000US-00703474.
 XX
 XX (UNGE/) UNGER E C.
 PA (MATS/) MATSUNAGA T O.
 PA (RAMA/) RAMASWAMI V.
 PA (ROMA/) ROMANOWSKI M J.
 XX
 XX Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
 PI WPI; 2003-208921/20.
 DR
 XX Targeted delivery system comprising a bioactive agent homogeneously
 PT dispersed in a targeted matrix is especially useful in cancer therapy.
 PT
 XX Disclosure; Page 13; 46pp; English.
 PS
 XX The invention relates to a composition comprising a bioactive agent
 CC homogeneously dispersed in a targeted matrix (polymer and targeting
 CC ligand). Also included are a targeted matrix for use as a delivery
 CC vehicle comprising a polymer associated with a targeting ligand,
 CC enhancing the bioavailability of an agent comprising administration of
 CC the composition and treating cancer comprising administration of the
 CC novel composition. The method is useful for targeted delivery of a drug,
 CC especially in cancer therapy. The targeting ligand may be a peptide.
 CC Examples of targeting peptides are disclosed including cathepsin-D
 CC substrate peptides, peptides targeting receptors in the brain and kidney,
 CC peptides recognising fibronectin- and vitronectin-binding integrins,
 CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
 CC peptides targeting the angiogenic endothelium of solid tumours, tissue
 CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
 CC adrenal gland and retina), and cationic cancer-targeting peptides. The
 CC present sequence is a peptide targeting ligand disclosed in the invention
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 62; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RLCRIWIRVCR 12
 Db 1 RLCRIWIRVCR 12
 RESULT 14
 AAE34432
 ID AAE34432 standard; peptide; 12 AA.
 XX
 AC AAE34432;
 XX
 XX 14-MAY-2003 (first entry)
 DT
 XX Cow batenecin peptide.
 DE
 XX Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;
 KW cow; batenecin.
 KW
 XX Bos taurus.
 OS
 XX WO200295076-A2.
 PN
 XX 28-NOV-2002.
 PD
 XX 17-MAY-2002; 2002WO-JP004800.
 PF

SQ Sequence 12 AA;
 Query Match 100.0%; Score 62; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLCRIWIRVCR 12
 |||||
 Db 1 RLCRIWIRVCR 12

RESULT 17
 ADX08379
 ID ADX08379 standard; peptide; 12 AA.
 XX
 AC ADX08379;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE BNP-1 antimicrobial peptide SEQ ID NO 52.
 XX
 KW vulnary; antiulcer; antiinflammatory; gastrointestinal-gen.;
 KW expression; vector; wound healing; vulnary; injury; antimicrobial.
 XX
 OS Bos taurus.
 XX
 PN WO2005012492-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 30-JUL-2004; 2004WO-US024627.
 XX
 PR 01-AUG-2003; 2003US-0491869P.
 PR 08-AUG-2003; 2003US-0493664P.
 PR 30-JUL-2004; 51US-00493664.
 XX
 PA (STRA-) STRATATECH CORP.
 XX
 PI Centanni JM, Allen-Hoffmann L;
 XX
 DR WPI; 2005-142888/15.
 XX
 PT Providing cells expressing heterologous keratinocyte growth factor-2 (I),
 PT which is useful to treat wounds e.g. ulcerative colitis, comprises
 PT introducing a vector comprising a DNA that encodes (I) to a host cell and
 PT culturing the host cell.
 XX
 PS Disclosure; SEQ ID NO 52; 116pp; English.
 XX
 CC The invention describes providing cells expressing heterologous
 CC keratinocyte growth factor-2 (KGF-2) (I) comprising providing a host cell
 CC consisting of primary keratinocytes and immortalized keratinocytes
 CC and an expression vector comprising a DNA sequence encoding (I) operably
 CC linked to a regulatory sequence; introducing the expression vector to
 CC (II); and culturing (II) under conditions such that (I) is expressed.
 CC Also described are: (II) produced by the novel method; a composition
 CC comprising (II) expressing (I); a method of treating wounds; a vector
 CC comprising a keratinocyte specific promoter operably linked to a DNA
 CC sequence encoding KGF-2 or an antimicrobial polypeptide; a host cell
 CC comprising the vector; a human tissue comprising the host cell, which
 CC comprises the vector; a method for providing a skin equivalent expressing
 CC an exogenous antimicrobial polypeptide; a composition comprising
 CC keratinocytes expressing an exogenous antimicrobial polypeptide; a method
 CC for providing a human tissue expressing an exogenous KGF-2 and an
 CC exogenous antimicrobial polypeptide; a method of selecting cells with
 CC increased pluripotency or multipotency relative to a population
 CC comprising providing a population of cells and electroporating the cells
 CC under conditions such that electroporated cells with increased
 CC pluripotency or multipotency relative to the population of cells are
 CC selected; a population of cells generated by the method; a population of
 CC cells generated by the method; a method of selecting keratinocytes with
 CC holoclone or meroclone cell morphology comprising providing a population
 CC of keratinocytes and electroporating the keratinocytes under conditions

CC such that electroporated keratinocytes with holoclone or meroclone cell
 CC morphology are selected; and a keratinocyte population generated by the
 CC method. (I) is useful to treat wounds such as venous ulcers, diabetic
 CC ulcers, pressure ulcers, burns, ulcerative colitis, mucousal injuries,
 CC internal injuries or external injuries. The method is useful to increase
 CC practitioners' success in healing wounds and/or accelerate the rate of
 CC chronic wound healing. The NIKS cells is genetically uniform, pathogen
 CC free human keratinocytes. This is the amino acid sequence of an
 CC antimicrobial peptide of the invention.
 XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 9; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIWIRVCR 12
 |||||
 Db 1 RLCRIWIRVCR 12

RESULT 18
 ADY67437
 ID ADY67437 standard; peptide; 12 AA.
 XX
 AC ADY67437;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Tumor cell targeting peptide - SEQ ID 676.
 XX
 KW cancer; cytostatic; delivery mechanism; drug delivery.
 XX
 OS Unidentified.
 XX
 PN US2005058603-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 03-MAY-2004; 2004US-00838289.
 XX
 PR 02-MAY-2003; 2003US-0467389P.
 PR 12-SEP-2003; 2003US-0502429P.
 XX
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 XX
 PI Gao J, Ai H;
 XX
 DR WPI; 2005-240846/25.
 XX

PT Polymeric nanoshells useful for delivery of bioactive agents such as
 PT therapeutic (e.g., antineoplastic drugs) or diagnostic agents, comprises
 PT biocompatible polymer layers comprising charged organic polymers, that
 PT define hollow core.
 XX

PS Disclosure; SEQ ID NO 676; 177pp; English.

XX The invention comprises polymeric nanoshells consisting of two or more
 CC biocompatible polymer layers that define a hollow core, the polymeric
 CC nanoshells are between 50-1000 nm in diameter and one or more of the
 CC polymer layers contains charged organic polymers. The polymeric
 CC nanoshells of the invention are useful for treating cancer. The polymeric
 CC nanoshells of the invention are also useful for delivering diagnostic
 CC agents or drugs to specific tissues. The present amino acid sequence
 CC represents a tumor cell targeting peptide that was used in the
 CC exemplification of the invention.
 XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 9; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RLCRIWVVR 12
Db      1 RLCRIWVVR 12

RESULT 19
AAY67340
ID      AAY67340 standard; peptide; 14 AA.
XX
XX      AC      AAY67340;
XX
XX      DT      11-APR-2000 (first entry)
XX
XX      DE      Antimicrobial batenecin peptide derivative BAC 2R.
XX
XX      KW      Batenecin; antimicrobial activity; cytostatic; antiproliferative;
XX      KW      antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
XX      KW      cell proliferative disorder; anticancer agent; BAC 2R.
XX
XX      OS      Synthetic.
XX
XX      PN      WO9960016-A2.
XX
XX      PD      25-NOV-1999.
XX
XX      PF      20-MAY-1999; 99WO-CA000414.
XX
XX      PR      20-MAY-1998; 98US-00082420.
XX
XX      PA      (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX      PI      Hancock REW, Wu M;
XX
XX      DR      WPI; 2000-126379/11.
XX
XX      PT      Antimicrobial peptide useful for inhibiting the growth of bacteria and as
XX      PT      anticancer agents.
XX
XX      PS      Claim 1; Page 36; 52pp; English.
XX
XX      CC      This sequence represents a derivative of the bovine batenecin peptide.
XX      CC      Batenecin is an antimicrobial cationic peptide, with antimicrobial
XX      CC      activity. The invention relates to isolated antimicrobial peptides (see
XX      CC      AAY67330-Y67347) derived from batenecin, and includes analogues,
XX      CC      derivatives, amidated variations and conservative variation. The peptides
XX      CC      have antimicrobial, cytostatic, antiproliferative, antiviral, and
XX      CC      antifungal activities. The antimicrobial peptides are useful for
XX      CC      inhibiting the growth of bacteria including both gram positive and
XX      CC      negative species including Escherichia coli, Pseudomonas aeruginosa and
XX      CC      Salmonella typhimurium. The peptides can be used to inhibit endotoxaemia
XX      CC      or sepsis associated disorders, such as septic shock. The peptides can
XX      CC      also be used to inhibit the growth of a eukaryotic cell, especially an
XX      CC      animal, neoplastic cell, in particular a glioblastoma cell. The peptides
XX      CC      can also be used to inhibit a cell proliferation-associated disorder
XX
XX      SQ      Sequence 14 AA;
XX
XX      Query Match      100.0%; Score 62; DB 3; Length 14;
XX      Best Local Similarity 100.0%; Pred. No. 0.0032;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLCRIWVVR 12
Db      2 RLCRIWVVR 13

RESULT 20
AAY67347
ID      AAY67347 standard; peptide; 18 AA.
XX
XX      AC      AAY67347;
XX
XX      DT      11-APR-2000 (first entry)

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```

XX      DE      Antimicrobial batenecin peptide derivative BAC 3I, 3V.
XX
XX      KW      Batenecin; antimicrobial activity; cytostatic; antiproliferative;
XX      KW      antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
XX      KW      cell proliferative disorder; anticancer agent; BAC 3I 3V.
XX
XX      OS      Synthetic.
XX
XX      PN      WO9960016-A2.
XX
XX      PD      25-NOV-1999.
XX
XX      PF      20-MAY-1999; 99WO-CA000414.
XX
XX      PR      20-MAY-1998; 98US-00082420.
XX
XX      PA      (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX      PI      Hancock REW, Wu M;
XX
XX      DR      WPI; 2000-126379/11.
XX
XX      PT      Antimicrobial peptide useful for inhibiting the growth of bacteria and as
XX      PT      anticancer agents.
XX
XX      PS      Claim 1; Page 36; 52pp; English.
XX
XX      CC      This sequence represents a derivative of the bovine batenecin peptide.
XX      CC      Batenecin is an antimicrobial cationic peptide, with antimicrobial
XX      CC      activity. The invention relates to isolated antimicrobial peptides (see
XX      CC      AAY67330-Y67347) derived from batenecin, and includes analogues,
XX      CC      derivatives, amidated variations and conservative variation. The peptides
XX      CC      have antimicrobial, cytostatic, antiproliferative, antiviral, and
XX      CC      antifungal activities. The antimicrobial peptides are useful for
XX      CC      inhibiting the growth of bacteria including both gram positive and
XX      CC      negative species including Escherichia coli, Pseudomonas aeruginosa and
XX      CC      Salmonella typhimurium. The peptides can be used to inhibit endotoxaemia
XX      CC      or sepsis associated disorders, such as septic shock. The peptides can
XX      CC      also be used to inhibit the growth of a eukaryotic cell, especially an
XX      CC      animal, neoplastic cell, in particular a glioblastoma cell. The peptides
XX      CC      can also be used to inhibit a cell proliferation-associated disorder
XX
XX      SQ      Sequence 18 AA;
XX
XX      Query Match      100.0%; Score 62; DB 3; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 0.004;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLCRIWVVR 12
Db      1 RLCRIWVVR 12

RESULT 21
ABB07704
ID      ABB07704 standard; peptide; 155 AA.
XX
XX      AC      ABB07704;
XX
XX      DT      10-JUN-2002 (first entry)
XX
XX      DE      Bovine peptide antibiotic batenecin precursor sequence.
XX
XX      KW      Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
XX      KW      antigen presenting cell; adjuvant; bovine; antibiotic; batenecin.
XX
XX      OS      Bos sp.
XX
XX      PN      WO200213857-A2.
XX
XX      PD      21-FEB-2002.
XX

```

PF 17-AUG-2001; 2001WO-EP009529.
 XX
 PR 17-AUG-2000; 2000AT-00001416.
 XX
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
 XX WPI; 2002-269154/31.
 DR
 XX Vaccine for active immunization or for preparing an adjuvant for
 PT enhancing an immune response to at least one antigen, comprises at least
 PT one antigen and at least one cathelicidin derived antimicrobial peptide.
 XX
 PS Disclosure; Fig 1; 65pp; English.
 XX
 CC The invention relates to a vaccine comprising at least one antigen and at
 CC least one cathelicidin derived antimicrobial peptide or its derivative.
 CC The vaccine is useful for active immunization, especially of humans or
 CC animals without protection against the specific antigen. The cathelicidin
 CC derived antimicrobial peptide is useful in the preparation of an adjuvant
 CC for enhancing the immune response to at least one antigen, where the
 CC adjuvant enhances the uptake of at least one antigen in antigen
 CC presenting cells (APC), and the adjuvant is added to the vaccine.
 CC Sequences ABB07701-07 represent cathelicidin proteins form various
 CC species
 XX
 SQ Sequence 155 AA;
 Query Match 100.0%; Score 62; DB 5; Length 155;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLCRIWIRVCR 12
 DB |||||
 144 RLCRIWIRVCR 155
 RESULT 22
 AAU90993
 ID AAU90993 standard; peptide; 155 AA.
 AC AAU90993;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Transplant media associated antimicrobial peptide #29.
 XX
 KW Transplant; antimicrobial peptide; pore forming agent;
 KW cell surface receptor binding compound; kidney transplant; cardioplegia;
 KW organ transplant; transplant rejection.
 XX
 OS Bos taurus.
 XX
 PN WO200209738-A1.
 XX
 PD 07-FEB-2002.
 XX
 PF 27-JUL-2001; 2001WO-US023785.
 XX
 PR 28-JUL-2000; 2000US-0221632P.
 PR 17-NOV-2000; 2000US-0249602P.
 PR 15-MAY-2001; 2001US-0290932P.
 XX
 PA (MURP/) MURPHY C J.
 XX
 PI Murphy CJ, Reid TW, Meanulty JF;
 XX WPI; 2002-268995/31.
 DR
 XX Media comprising antimicrobial polypeptides or pore forming agents and/or
 PT cell surface receptor binding compounds useful for the storage and
 PT preservation of organs prior to transplant.

XX
 PS Disclosure; Page 26; 78pp; English.
 XX
 CC The invention describes new transplant compositions comprising
 CC antimicrobial polypeptides or pore forming agents and/or cell surface
 CC receptor binding compounds. The media is capable of extending the
 CC preservation period past 72 hours and can provide organs with increased
 CC functionality upon transplant. animals receiving kidneys stored in the
 CC media of the present invention for either three or four days had serum
 CC creatinine levels of less than half of those observed in control animals
 CC receiving kidneys stored in UW solution (defined in the specification)
 CC alone. Lower serum creatinine levels are indicative of healthier kidneys
 CC and a more preferable prognosis for the transplant patient. The media of
 CC the invention are useful for decreasing the incidence and/or severity of
 CC delayed graft function in patients receiving transplanted kidneys stored
 CC and/or treated in the media. The media may also be used in procedures
 CC such as cardioplegia. It is contemplated that transplant of healthier
 CC organs leads to a decrease in chronic rejection. This sequence represents
 CC an antimicrobial peptide studied in the development of the transplant
 CC media
 XX
 SQ Sequence 155 AA;
 Query Match 100.0%; Score 62; DB 5; Length 155;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLCRIWIRVCR 12
 DB |||||
 144 RLCRIWIRVCR 155
 RESULT 23
 ADX08371
 ID ADX08371 standard; protein; 155 AA.
 XX
 AC ADX08371;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Bactenecin precursor antimicrobial peptide SEQ ID NO 44.
 XX
 KW vulnery; antiulcer; antiinflammatory; gastrointestinal-gen.;
 KW expression; vector; wound healing; vulnery; injury; antimicrobial.
 XX
 OS Bos taurus.
 XX
 PN WO2005012492-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 30-JUL-2004; 2004WO-US024627.
 XX
 PR 01-AUG-2003; 2003US-0491869P.
 PR 08-AUG-2003; 2003US-0493664P.
 PR 30-JUL-2004; 51US-00493664.
 XX
 PA (STRA-) STRATATECH CORP.
 XX
 PI Centauni JM, Allen-Hoffmann L;
 XX WPI; 2005-142888/15.
 DR
 XX Providing cells expressing heterologous keratinocyte growth factor-2 (I),
 PT which is useful to treat wounds e.g. ulcerative colitis, comprises
 PT introducing a vector comprising a DNA that encodes (I) to a host cell and
 PT culturing the host cell.
 XX
 PS Disclosure; SEQ ID NO 44; 116pp; English.
 XX
 CC The invention describes providing cells expressing heterologous
 CC keratinocyte growth factor-2 (KGF-2) (I) comprising providing a host cell
 CC (II) consisting of primary keratinocytes and immortalized keratinocytes

CC and an expression vector comprising a DNA sequence encoding (I) operably
 CC linked to a regulatory sequence; introducing the expression vector to
 CC (II); and culturing (II) under conditions such that (I) is expressed.
 CC Also described are: (II) produced by the novel method; a composition
 CC comprising (II) expressing (I); a method of treating wounds; a vector
 CC comprising a keratinocyte specific promoter operably linked to a DNA
 CC sequence encoding KGF-2 or an antimicrobial polypeptide; a host cell
 CC comprising the vector; a human tissue comprising the host cell, which
 CC comprises the vector; a method for providing a skin equivalent comprising
 CC an exogenous antimicrobial polypeptide; a composition comprising
 CC keratinocytes expressing an exogenous antimicrobial polypeptide; a method
 CC for providing a human tissue expressing an exogenous KGF-2 and an
 CC exogenous antimicrobial polypeptide; a method of selecting cells with
 CC increased pluripotency or multipotency relative to a population
 CC comprising providing a population of cells and electroporating the cells
 CC under conditions such that electroporated cells with increased
 CC pluripotency or multipotency relative to the population of cells are
 CC selected; a population of cells generated by the method; a population of
 CC cells generated by the method; a method of selecting keratinocytes with
 CC holoclone or meroclone cell morphology comprises providing a population
 CC of keratinocytes and electroporating the keratinocytes under conditions
 CC such that electroporated keratinocytes with holoclone or meroclone cell
 CC morphology are selected; and a keratinocyte population generated by the
 CC method. (I) is useful to treat wounds such as venous ulcers, diabetic
 CC ulcers, pressure ulcers, burns, ulcerative colitis, mucosal injuries,
 CC internal injuries or external injuries. The method is useful to increase
 CC practitioners's success in healing wounds and/or accelerate the rate of
 CC chronic wound healing. The NTKs cells is genetically uniform, pathogen
 CC free human keratinocytes. This is the amino acid sequence of an
 CC antimicrobial peptide of the invention.

XX SQ Sequence 155 AA;

Query Match 100.0%; Score 62; DB 9; Length 155;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVRCR 12
 |||||
 Db 144 RLCRIWVRCR 155

RESULT 24

ADR82249
 ID ADR82249 standard; peptide; 12 AA.

XX AC ADR82249;

DT 16-DEC-2004 (first entry)

XX Cell permeation peptide beta-defensin.

XX antileptic; cardiac; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cytosolic; anticonvulsant; nootropic; muscle; anti-HIV;
 KW RNA interference; RNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease;
 KW spinocerebellar ataxia; viral disease; AIDS; cell permeation peptide;
 KW beta defensin.

XX OS Unidentified.

XX PN W02004080406-A2.

XX 23-SEP-2004.

XX 08-MAR-2004; 2004WO-US0007070.

XX 07-MAR-2003; 2003US-0452682P.

PR 12-MAR-2003; 2003US-0454265P.

PR 13-MAR-2003; 2003US-0454962P.
 PR 13-MAR-2003; 2003US-0455050P.
 PR 14-APR-2003; 2003US-0462894P.
 PR 17-APR-2003; 2003US-0463772P.
 PR 25-APR-2003; 2003US-0465665P.
 PR 25-APR-2003; 2003US-0465802P.
 PR 09-MAY-2003; 2003US-0469612P.
 PR 08-AUG-2003; 2003US-0493386P.
 PR 11-AUG-2003; 2003US-0494597P.
 PR 26-SEP-2003; 2003US-0506341P.
 PR 09-OCT-2003; 2003US-0510246P.
 PR 10-OCT-2003; 2003US-0510318P.
 PR 07-NOV-2003; 2003US-0518453P.

XX (ALNY-) ALNYLAM PHARM.

XX Manoharan M, Bumcrot D;

XX WI; 2004-677362/66.

XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 PT disease, diabetes, cancer or neurological disease, comprises sense
 PT sequence and antisense sequence which has specific modifications.

PS Disclosure; SEQ ID NO 6748; 378pp; English.

CC The invention describes a RNA interference (RNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (MI) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity, a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (MI)
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
 CC inhibit hepatic glucose production or for treating glucose-metabolism-
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This is the amino
 CC acid sequence of a cell permeation peptide that can be used as a ligand
 CC to increase the uptake of iRNA's.

XX SQ Sequence 12 AA;

Query Match 90.3%; Score 56; DB 8; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLCRIWVRCR 12
 |||||
 Db 1 RLCRIWVRCR 12

RESULT 25

ADT61094
 ID ADT61094 standard; peptide; 12 AA.

XX AC ADT61094;

XX 13-JAN-2005 (first entry)

XX DE Novel interfering RNA (iRNA)-related cell permeation peptide SeqID19.
 XX KW interfering RNA; iRNA; kidney; stabilising modification; nephrotropic;
 KW antidiabetic; cytostatic; vasotropic; antiinflammatory; dermatological;
 KW immunosuppressive; antisense therapy; kidney disorder;
 KW ureter obstruction; diabetes; proteinuria; renal carcinoma;
 KW Fanconi's syndrome; Bartter's syndrome; kidney transplant; shock;
 KW renal vascular hypertension; glomerular sclerosis; glomerular nephritis;
 KW systemic lupus erythematosus; HIV-associated nephropathy; renal fibrosis;
 KW inflammatory disease; necessary renal transplantation; cell permeation.
 XX OS Unidentified.
 XX KW WO200409108-A2.
 XX PD 21-OCT-2004.
 XX PF 05-APR-2004; 2004WO-US010586.
 XX PR 03-APR-2003; 2003US-0460783P.
 XX PR 14-APR-2003; 2003US-0462894P.
 XX PR 17-APR-2003; 2003US-0463772P.
 XX PR 25-APR-2003; 2003US-0465665P.
 XX PR 25-APR-2003; 2003US-0465802P.
 XX PR 09-MAY-2003; 2003US-0469612P.
 XX PR 08-AUG-2003; 2003US-0493986P.
 XX PR 11-AUG-2003; 2003US-0494597P.
 XX PR 15-SEP-2003; 2003US-0503414P.
 XX PR 26-SEP-2003; 2003US-0506341P.
 XX PR 09-OCT-2003; 2003US-0510246P.
 XX PR 10-OCT-2003; 2003US-0510318P.
 XX PR 07-NOV-2003; 2003US-0518453P.
 XX PR 08-MAR-2004; 2004WO-US007070.
 XX PA (ALNY-) ALNYLAM PHARM.
 XX XX Manoharan M;
 XX PI WPI; 2004-748749/73.
 XX DR Interfering RNA agent useful for treating subject having or at risk for
 XX PT having disorder of kidney such as ureter obstruction, or diabetes,
 XX PT comprises sense sequence, and antisense sequence, that targets RNA
 XX PT expressed in kidney.
 XX PS Disclosure; SEQ ID NO 19; 252pp; English.
 XX CC This invention relates to a novel interfering RNA (iRNA) agent comprising
 CC a sense sequence, and an antisense sequence, which targets an RNA
 CC expressed in kidney, where the agent has a stabilising modification. The
 CC invention may be useful for the production of compounds with a
 CC nephrotropic, antidiabetic, cytostatic, vasotropic, antiinflammatory,
 CC dermatological or immunosuppressive activity through antisense therapy.
 CC The invention is useful for treating a subject having or at risk for
 CC having a disorder of the kidney such as ureter obstruction, diabetes,
 CC proteinuria, renal carcinoma, Fanconi's syndrome and Bartter's syndrome,
 CC where the iRNA is administered before, during, or after a kidney
 CC transplant. The iRNA may be administered to a subject in shock and is
 CC useful for treating renal vascular hypertension, glomerular sclerosis,
 CC glomerular nephritis, systemic lupus erythematosus, HIV-associated
 CC nephropathy, renal fibrosis, or inflammatory diseases that may be
 CC eventually lead to necessary renal transplantation. The present sequence
 CC is that of a cell permeation peptide which was used during the
 CC illustration of the iRNA agents of the invention.
 XX SQ Sequence 12 RA;
 Query Match 90.3%; Score 56; DB 8; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RLCRIVVIRVCR 12

Db 1 RLCRIVVIRVCR 12
 RESULT 26
 ADT86670
 ID ADT86670 standard, peptide; 12 AA.
 XX AC ADT86670;
 XX DT 13-JAN-2005 (first entry)
 XX DE Bactenecin cell permeation peptide.
 XX KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 KW interference RNA; iRNA; cholesterol moiety; apoB; glucose-6-phosphatase;
 KW lipid metabolism; cholesterol imbalance; dyslipidaemia;
 KW familial combined hyperlipidaemia; acquired hyperlipidaemia;
 KW hypercholesterolaemia; statin-resistant hypercholesterolaemia;
 KW coronary artery disease; coronary heart disease; atherosclerosis;
 KW hepatic glucose production; glucose-metabolism-related disorder;
 KW type-2 diabetes; glitaxone-resistant diabetes; cell permeation peptide;
 KW bactenecin.
 XX OS Unidentified.
 XX XX WO2004091515-A2.
 XX PD 28-OCT-2004.
 XX PF 09-APR-2004; 2004WO-US011255.
 XX PR 09-APR-2003; 2003US-0462097P.
 XX PR 10-APR-2003; 2003US-0461915P.
 XX PR 14-APR-2003; 2003US-0462894P.
 XX PR 17-APR-2003; 2003US-0463772P.
 XX PR 25-APR-2003; 2003US-0465665P.
 XX PR 25-APR-2003; 2003US-0465802P.
 XX PR 09-MAY-2003; 2003US-0493986P.
 XX PR 08-AUG-2003; 2003US-0494597P.
 XX PR 11-AUG-2003; 2003US-0506341P.
 XX PR 26-SEP-2003; 2003US-0510246P.
 XX PR 09-OCT-2003; 2003US-0510318P.
 XX PR 10-OCT-2003; 2003US-0510318P.
 XX PR 07-NOV-2003; 2003US-0518453P.
 XX PR 08-MAR-2004; 2004WO-US007070.
 XX PR 05-APR-2004; 2004WO-US010586.
 XX PA (ALNY-) ALNYLAM PHARM INC.
 XX XX Manoharan M, Elbashir S, Harborth J;
 XX PI WPI; 2004-766693/75.
 XX DR New interference RNA agent comprising sense sequence and antisense
 XX PT sequence having cholesterol moieties, useful for reducing apoB-100 levels
 XX PT or glucose-6-phosphatase levels.
 XX PS Disclosure; SEQ ID NO 6712; 324pp; English.
 XX CC The invention describes an interference RNA (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequence
 CC comprises one or more cholesterol moieties, and the antisense sequence
 CC targets a human gene sequence. The following are disclosed: a
 CC pharmaceutical composition comprising (I); and a device for administering
 CC (I) into a patient. (I) is useful for reducing apoB-100 levels or glucose
 CC -6-phosphatase levels in a subject. (I) targets a sequence identical to
 CC any one of sequences as given in the specification. (I) comprises a
 CC cholesterol moiety. The cholesterol moiety is coupled to a sense strand.
 CC (I) further comprises a second cholesterol moiety. The second cholesterol
 CC moiety is coupled to a sense strand. (I) has 21 or more nucleotides. The
 CC duplex region of (I) is 19 nucleotides in length. The subject is
 CC suffering from a disorder having elevated or otherwise unwanted

CC expression of apo-B-100, elevated or otherwise unwanted levels of
 CC cholesterol, and/or dysregulation of lipid metabolism. The disorder is
 CC chosen from HDL/LDL cholesterol imbalance, dyslipidaemia (e.g., familial
 CC combined hyperlipidaemia or acquired hyperlipidaemia),
 CC hypercholesterolaemia, statin-resistant hypercholesterolaemia, coronary
 CC artery disease, coronary heart disease and atherosclerosis, preferably
 CC statin-resistant hypercholesterolaemia. (I) is administered to a subject
 CC to inhibit hepatic glucose production or for treating glucose-metabolism
 CC related disorders e.g., type-2 diabetes or glitazone-resistant diabetes.
 CC (I) has endonuclease or exonuclease resistance. This is the amino acid
 CC sequence of a cell permeation peptide that can be attached to iRNA's to
 CC enhance cellular recognition and absorption of the iRNA's.

XX Sequence 12 AA;

Query Match 90.3%; Score 56; DB 8; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLCRIWVVR 12
 Db 1 RKCRIVVVR 12

RESULT 27

ADU67508
 ID ADU67508 standard; peptide, 12 AA.

AC ADU67508;

XX 27-JAN-2005 (first entry)

XX Bactencin peptide for modified iRNA agent.

XX cytostatic; antirheumatic; antiarthritic; ophthalmological; anti-HIV;
 KW neuroprotective; interfering RNA; iRNA; gene silencing; gene regulation;
 KW cancer; rheumatoid arthritis; retinal neovascularization;
 KW viral infection; viral hemorrhagic fever; neurological disease;
 KW respiratory tract infection; poliovirus infection;
 KW variola virus infection; ribose replacement modification subunit.

XX Unidentified.

OS WO2004094595-A2.

XX 04-NOV-2004.

XX 16-APR-2004; 2004WO-US011829.

XX 17-APR-2003; 2003US-0463772P.

XX 25-APR-2003; 2003US-0465665P.

XX 25-APR-2003; 2003US-0465802P.

XX 09-MAY-2003; 2003US-0469612P.

XX 08-AUG-2003; 2003US-0493986P.

XX 11-AUG-2003; 2003US-0494597P.

XX 15-SEP-2003; 2003US-0503414P.

XX 26-SEP-2003; 2003US-0506341P.

XX 09-OCT-2003; 2003US-0510246P.

XX 10-OCT-2003; 2003US-0510318P.

XX 07-NOV-2003; 2003US-0518453P.

XX 08-MAR-2004; 2004WO-US007070.

XX 05-APR-2004; 2004WO-US010586.

XX 09-APR-2004; 2004WO-US011255.

XX (ALNY-) ALNYLAM PHARM INC.

PT entrance into cell.

XX Disclosure; SEQ ID NO 13; 309pp; English.

XX The invention relates to an interfering RNA (iRNA) agent (A1), comprising
 CC a first and a second strand, where at least one monomer contains non-
 CC ribose subunit is incorporated into at least one of the strands or where
 CC at least one subunit is derivatized with a lipophilic moiety which
 CC enhances entrance into a cell. (A1) is useful for silencing a target gene
 CC which involves providing (A1) to which a lipophilic moiety is conjugated,
 CC to a cell. (A1) is administered to an organism. (A1) is contacted with a
 CC cell which is outside an organism. The cell is a cell of a cell line.
 CC (A1) which is conjugated to a lipophilic moiety, is administered to an
 CC organism, or contacted with a cell which is not part of an organism, is
 CC administered in the absence of or in a reduced amount of other reagents
 CC that facilitate or enhance delivery. Preferably the other reagents are
 CC absent. (A1) is useful for modulating expression of a target gene in a
 CC gene in a subject (all claimed). (A1) is useful for silencing genes in a
 CC various cells such as epithelial cell or mesodermal cell, neural cell,
 CC keratinocyte, lymphoma or a leukemia cell, mast cell, etc. (A1) is useful
 CC for treating e.g. lung cancer, colon cancer, chronic myelogenous
 CC leukemia, Burkitt's lymphoma, ovarian, prostate or breast cancers, skin
 CC cancers, Non-Hodgkin lymphoma, cervical cancer, basal cell carcinoma,
 CC adenocarcinoma or hepatocellular carcinoma, pancreatic cancers,
 CC colorectal adenocarcinoma, liver cancer, esophageal squamous cell
 CC carcinoma, male breast carcinoma (MBC), ovarian carcinoma, gall bladder
 CC cancer, squamous cell carcinoma, acute leukemias, Ewing Sarcoma, Myxoid
 CC liposarcoma, rheumatoid arthritis, retinal neovascularization, viral
 CC infection (human papilloma virus (HPV), HIV, HBV), Kaposi's sarcoma,
 CC multicentric Castleman's disease and AIDS-associated primary effusion
 CC lymphoma, viral hemorrhagic fever or neurological disease, respiratory
 CC tract infection, polio and smallpox. The incorporation of ribose
 CC replacement modification subunit (RRMS) in (A1) confers new properties
 CC Other moieties may also be attached to the RRMS moiety including ligands
 CC and targeting peptides. This sequence corresponds to a targeting peptide
 CC which is a cell permeating peptide used to allow the iRNA entry into a
 CC cell.

XX Sequence 12 AA;

Query Match 90.3%; Score 56; DB 8; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLCRIWVVR 12

Db 1 RKCRIVVVR 12

RESULT 28

ADU26587
 ID ADU26587 standard; peptide, 12 AA.

XX ADU26587;

XX 27-JAN-2005 (first entry)

XX Cell permeation peptide #13 for oligo containing protected monomer.

XX cytostatic; antimicrobial; virucide; immunosuppressive; antiinflammatory;
 KW analgesic; neuroprotective; anticonvulsant; nootropic; gene silencing;
 KW RNA interference; cancer; viral infection; bacterial infection;
 KW amoeba infection; parasitic infection; fungal infection; inflammation;
 KW autoimmune disease; immune disorder; Huntingtons chorea;
 KW loss of heterozygosity; genetic disorder.

XX Unidentified.

XX WO2004094345-A2.

XX 04-NOV-2004.

PT comprises first and second strand having monomer containing non-ribose
 subunit or monomer derivatized with lipophilic moiety which enhances

PF 16-APR-2004; 2004WO-US011822.
 XX 17-APR-2003; 2003US-0463772P.
 PR 25-APR-2003; 2003US-0465665P.
 PR 25-APR-2003; 2003US-0465802P.
 PR 08-MAY-2003; 2003US-0469612P.
 PR 08-AUG-2003; 2003US-0493986P.
 PR 11-AUG-2003; 2003US-0494597P.
 PR 26-SEP-2003; 2003US-0506341P.
 PR 09-OCT-2003; 2003US-0510246P.
 PR 10-OCT-2003; 2003US-0510318P.
 PR 07-NOV-2003; 2003US-0518453P.
 PR 08-MAR-2004; 2004WO-US007070.
 PR 05-APR-2004; 2004WO-US001586.
 PR 09-APR-2004; 2004WO-US011255.
 XX (ALNY-) ALNYLAM PHARM INC.
 PA Manoharan M;
 XX MPI; 2004-804482/79.
 DR Novel protected monomers useful for preparing natural or modified
 PT oligoribonucleotides and for synthesizing iRNA agent that is useful for
 PT treating cancer and microbial infections.
 XX
 PS Disclosure; SEQ ID NO 13; 415pp; English.
 XX The invention relates to a novel protected monomer (MRL1). (MRL1) is useful
 CC for preparing natural or modified oligoribonucleotides or polymeric
 CC molecules and preparing an RNA e.g. an iRNA agent. The iRNA agent (A1) is
 CC useful for treating a subject at risk for or afflicted with unwanted cell
 CC proliferation e.g. lung cancer, breast cancer, prostate cancer, ovarian
 CC cancer, and leukemia, for treating a subject infected with a virus e.g.
 CC HIV, hepatitis B virus, and human papilloma virus, or at risk for or
 CC afflicted with a disease or disorder associated with viral infection,
 CC treating a subject infected with other pathogens e.g. bacterial, amoebic,
 CC parasitic or fungal pathogen, treating a subject with a disease or
 CC disorder associated with immune response e.g. inflammatory disease or
 CC autoimmune disease, treating a subject with acute or chronic pain,
 CC neurological disease or disorder, neurodegenerative trinucleotide repeat
 CC disorder e.g. Huntington disease and disorder associated with loss of
 CC heterozygosity (LOH) e.g. cancer. (A1) has ability to inhibit
 CC degradation, e.g. by nucleases. This sequence corresponds to a peptide
 CC fragment that can be used as a carrier peptide for oligonucleotides
 CC containing the novel monomers.
 XX
 SQ Sequence 12 AA;
 Query Match 90.3%; Score 56; DB 8; Length 12;
 Best Local Similarity 91.7%; Pred. NO. 0.025;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RLCRIVIRVCR 12
 Db 1 RKCRIIVIRVCR 12
 RESULT 29
 ADW25979
 ID ADW25979 standard; peptide; 12 AA.
 XX ADW25979;
 AC
 XX 07-APR-2005 (first entry)
 DT
 XX Bactenecin cell permeation peptide.
 DE
 XX neuroprotective; nootropic; antiparkinsonian; gene therapy;
 KW antisense therapy; expression; pharmaceutical; neurodegenerative disease;
 KW antiparkinsonian; neuroprotective; nootropic; bactenecin.
 XX
 OS Unidentified.

XX WO2005004794-A2.
 XX 20-JAN-2005.
 PD 09-JUN-2004; 2004WO-US018271.
 PF 09-JUN-2003; 2003US-0476947P.
 PR (ALNY-) ALNYLAM PHARM INC.
 XX Mayo Foundation For Medical Ed, Bumcrot D, Farrer MJ, Maraganore D;
 PI Vornlocher H;
 XX MPI; 2005-091965/10.
 DR
 XX New iRNA agent for treating neurodegenerative disorders comprises an
 PT antisense strand complementary to a nucleotide sequence of an alpha-
 PT synuclein RNA, and a sense strand complementary to hybridize to the
 PT antisense strand.
 XX Disclosure; SEQ ID NO 43; 190pp; English.
 PS The invention describes an iRNA agent comprising an antisense strand
 CC complementary to a nucleotide sequence of an alpha-synuclein (SNCA) RNA,
 CC and a sense strand complementary to hybridize to the antisense strand.
 CC Also described are: treating a human; a pharmaceutical composition
 CC comprising the above iRNA agent that targets the alpha-synuclein gene,
 CC and a pharmaceutical carrier; reducing the amount of SNCA RNA in a cell
 CC of a subject; making an iRNA agent; evaluating an iRNA agent that targets
 CC an SNCA nucleic acid; and evaluating an agent for the ability to inhibit
 CC SNCA expression. The composition and methods are useful for treating
 CC neurodegenerative diseases, such as synucleinopathy, Parkinson's disease,
 CC Alzheimer's disease, multiple system atrophy or Lewy body dementia. This
 CC is the amino acid sequence of a cell wall permeating peptide suitable for
 CC use delivering the siRNA's of the invention into cells.
 XX
 SQ Sequence 12 AA;
 Query Match 90.3%; Score 56; DB 9; Length 12;
 Best Local Similarity 91.7%; Pred. NO. 0.025;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RLCRIVIRVCR 12
 Db 1 RKCRIIVIRVCR 12
 RESULT 30
 RAY67332
 ID RAY67332 standard; peptide; 12 AA.
 XX RAY67332;
 AC
 XX 11-APR-2000 (first entry)
 DT
 XX Antimicrobial bactenecin peptide derivative BAC 1S-NH2.
 DE
 XX Bactenecin; antimicrobial activity; cytostatic; antiproliferative;
 KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
 KW cell proliferative disorder; anticancer agent; BAC 1S-NH2.
 XX
 OS Synthetic.
 XX WO9960016-A2.
 XX 25-NOV-1999.
 PD
 XX 20-MAY-1999; 99WO-CA000414.
 PF
 XX 20-MAY-1998; 98US-00082420.
 PR
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA


```

XX SQ Sequence 13 AA;
    Query Match      83.1%; Score 51.5; DB 3; Length 13;
    Best Local Similarity 92.3%; Pred. No. 0.14;
    Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 1 RLCRIV-VIRVCR 12
    ||||| |||||
Db 1 RLCRIVWVIRVCR 13

RESULT 33
AAAY67343
ID AAY67343 standard; peptide; 15 AA.
XX
AC AAY67343;
XX
XX 11-APR-2000 (first entry)
XX Antimicrobial batenecin peptide derivative BAC W, 2R.
DE
XX Batenecin; antimicrobial activity; cytostatic; antiproliferative;
KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
KW cell proliferative disorder; anticancer agent; BAC W 2R.
XX
XX Synthetic.
OS
XX WO9960016-A2.
FN
XX 25-NOV-1999.
PD
XX 20-MAY-1999; 99WO-CA000414.
PF
XX 20-MAY-1998; 98US-00082420.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Hancock REW, Wu M;
PI
XX WPI; 2000-126379/11.
DR
XX Antimicrobial peptide useful for inhibiting the growth of bacteria and as
PT anticancer agents.
XX
XX Claim 1; Page 36; 52pp; English.
XX
XX This sequence represents a derivative of the bovine batenecin peptide.
CC Batenecin is an antimicrobial cationic peptide, with antimicrobial
CC activity. The invention relates to isolated antimicrobial peptides (see
CC AAY67330-Y67347) derived from batenecin, and includes analogues,
CC derivatives, amidated variations and conservative variation. The peptides
CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
CC antifungal activities. The antimicrobial peptides are useful for
CC inhibiting the growth of bacteria including both gram positive and
CC negative species including Escherichia coli, Pseudomonas aeruginosa and
CC Salmonella typhimurium. The peptides can be used to inhibit endotoxaemia
CC or sepsis associated disorders, such as septic shock. The peptides can
CC also be used to inhibit the growth of a eukaryotic cell, especially an
CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
CC can also be used to inhibit a cell proliferation-associated disorder
XX
XX Sequence 15 AA;
    Query Match      83.1%; Score 51.5; DB 3; Length 15;
    Best Local Similarity 92.3%; Pred. No. 0.16;
    Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 1 RLCRIV-VIRVCR 12
    ||||| |||||
Db 2 RLCRIVWVIRVCR 14

RESULT 34
AAAY67334
ID AAY67334 standard; peptide; 12 AA.
XX
AC AAY67334;
XX
XX 11-APR-2000 (first entry)
XX Antimicrobial batenecin peptide derivative BAC R, P.
DE
XX Batenecin; antimicrobial activity; cytostatic; antiproliferative;
KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
KW cell proliferative disorder; anticancer agent; BAC R P.
XX
XX Synthetic.
OS
XX WO9960016-A2.
FN
XX 25-NOV-1999.
PD
XX 20-MAY-1999; 99WO-CA000414.
PF
XX 20-MAY-1998; 98US-00082420.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Hancock REW, Wu M;
PI
XX WPI; 2000-126379/11.
DR
XX Antimicrobial peptide useful for inhibiting the growth of bacteria and as
PT anticancer agents.
XX
XX Claim 1; Page 36; 52pp; English.
XX
XX This sequence represents a derivative of the bovine batenecin peptide.
CC Batenecin is an antimicrobial cationic peptide, with antimicrobial
CC activity. The invention relates to isolated antimicrobial peptides (see
CC AAY67330-Y67347) derived from batenecin, and includes analogues,
CC derivatives, amidated variations and conservative variation. The peptides
CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
CC antifungal activities. The antimicrobial peptides are useful for
CC inhibiting the growth of bacteria including both gram positive and
CC negative species including Escherichia coli, Pseudomonas aeruginosa and
CC Salmonella typhimurium. The peptides can be used to inhibit endotoxaemia
CC or sepsis associated disorders, such as septic shock. The peptides can
CC also be used to inhibit the growth of a eukaryotic cell, especially an
CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
CC can also be used to inhibit a cell proliferation-associated disorder
XX
XX Sequence 12 AA;
    Query Match      79.0%; Score 49; DB 3; Length 12;
    Best Local Similarity 83.3%; Pred. No. 0.32;
    Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RLCRIVVIRVCR 12
    ||||| |||||
Db 1 RRCPIVWVIRVCR 12

RESULT 35
AAAY67338
ID AAY67338 standard; peptide; 14 AA.
XX
AC AAY67338;
XX
XX 11-APR-2000 (first entry)
XX Antimicrobial batenecin peptide derivative BAC 3R, P.
DE
XX Batenecin; antimicrobial activity; cytostatic; antiproliferative;
KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;

```

KW cell proliferative disorder; anticancer agent; BAC 3R P.
 XX Synthetic.
 OS

XX WO9960016-A2.
 PN

XX 25-NOV-1999.
 PD

XX 20-MAY-1999; 99WO-CA000414.
 PF

XX 20-MAY-1998; 98US-00082420.
 PR

XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA

XX Hancock REW, Wu M;
 PI

XX WPI; 2000-126379/11.
 DR

XX Antimicrobial peptide useful for inhibiting the growth of bacteria and as
 PT anticancer agents.
 PT

XX Claim 1; Page 36; 52pp; English.
 XX

CC This sequence represents a derivative of the bovine batenecin peptide.
 CC Batenecin is an antimicrobial cationic peptide, with antimicrobial
 CC activity. The invention relates to isolated antimicrobial peptides (see
 CC AAY67330-Y67347) derived from batenecin, and includes analogues,
 CC derivatives, amidated variations and conservative variation. The peptides
 CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
 CC antifungal activities. The antimicrobial peptides are useful for
 CC inhibiting the growth of bacteria including both gram positive and
 CC negative species including Escherichia coli, Pseudomonas aeruginosa and
 CC Salmonella typhimurium. The peptides can be used to inhibit endotoxaemia
 CC or sepsis associated disorders, such as septic shock. The peptides can
 CC also be used to inhibit the growth of a eukaryotic cell, especially an
 CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
 CC can also be used to inhibit a cell proliferation-associated disorder
 CC

XX SQ Sequence 14 AA;

Query Match 79.0%; Score 49; DB 3; Length 14;
 Best Local Similarity 83.3%; Pred. No. 0.37;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12

Db 2 RRCPIVVIRVCR 13

RESULT 36

ABP71542
 ID ABP71542 standard; peptide; 11 AA.

XX AC ABP71542;

XX 29-MAY-2003 (first entry)
 DT

XX Bovine neutrophil peptide (BNP)-1 defensin peptide.
 DE

XX Magainin; antimicrobial; preservative; ophthalmological; eye treatment;
 KW contact lens; cecropin; bovine neutrophil peptide; BNP-1; defensin.
 KW

XX Bos sp.
 OS

XX WO2003006046-A1.
 PN

XX 23-JAN-2003.
 PD

XX 11-JUL-2002; 2002WO-US022238.
 PF

XX 13-JUL-2001; 2001US-00904753.
 PR

XX (ALLR) ALLERGAN INC.
 PA

XX Lyons RT;
 PI

XX WPI; 2003-229449/22.
 DR

XX Ophthalmic composition for eye care and contact lens care, comprises
 PT magainin antimicrobial peptide or its analog as a preservative.
 PT

XX Disclosure; Page 11; 43pp; English.
 XX

CC The invention provides an ophthalmic composition comprising an
 CC antimicrobial peptide mimetic, especially a component such as magainin
 CC antimicrobial peptide and/or analogue of magainin antimicrobial peptide
 CC present in an amount effective as a preservative in the composition, and
 CC includes a therapeutically effective component. Magainin antimicrobial
 CC peptides display a reduced eye irritation compared to existing
 CC preservatives for ophthalmic compositions. The peptides are highly water-
 CC soluble allowing effective antimicrobial action in oil-in-water emulsion.
 CC The preserved ophthalmic composition is useful for eye treatment, may be
 CC used as a surgical irrigant, and to care for contact lenses. The present
 CC sequence represents an antimicrobial defensin peptide of bovine
 CC neutrophil peptide (BNP)-1
 CC

XX SQ Sequence 11 AA;

Query Match 76.6%; Score 47.5; DB 6; Length 11;
 Best Local Similarity 91.7%; Pred. No. 0.52;
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RLCRIVVIRVCR 12

Db 1 RLCC-VVIRVCR 11

RESULT 37

AAV67335

ID AAY67335 standard; peptide; 12 AA.

XX AC AAY67335;

XX 11-APR-2000 (first entry)
 DT

XX Antimicrobial batenecin peptide derivative BAC 2I-NH2.
 DE

XX Batenecin; antimicrobial activity; cytostatic; antiproliferative;
 KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
 KW cell proliferative disorder; anticancer agent; BAC 2I-NH2.
 KW

XX Synthetic.
 OS

XX WO9960016-A2.
 PN

XX 25-NOV-1999.
 PD

XX 20-MAY-1999; 99WO-CA000414.
 PF

XX 20-MAY-1998; 98US-00082420.
 PR

XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA

XX Hancock REW, Wu M;
 PI

XX WPI; 2000-126379/11.
 DR

XX Antimicrobial peptide useful for inhibiting the growth of bacteria and as
 PT anticancer agents.
 PT

XX Claim 1; Page 36; 52pp; English.
 XX

CC This sequence represents a derivative of the bovine batenecin peptide.
 CC Batenecin is an antimicrobial cationic peptide, with antimicrobial
 CC activity. The invention relates to isolated antimicrobial peptides (see
 CC AAY67330-Y67347) derived from batenecin, and includes analogues,
 CC

CC derivatives, amidated variations and conservative variation. The peptides
 CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
 CC antifungal activities. The antimicrobial peptides are useful for
 CC inhibiting the growth of bacteria including both gram positive and
 CC negative species including *Escherichia coli*, *Pseudomonas aeruginosa* and
 CC *Salmonella typhimurium*. The peptides can be used to inhibit endotoxaemia
 CC or sepsis associated disorders, such as septic shock. The peptides can
 CC also be used to inhibit the growth of a eukaryotic cell, especially an
 CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
 CC can also be used to inhibit a cell proliferation-associated disorder

XX SQ Sequence 12 AA;

Query Match 72.6%; Score 45; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.4; Mismatches 0; Gaps 0;
 Matches 9; Conservative 1; Indels 2;

OY 1 RLCRIWVIRVCR 12
 |:|||||||
 Db 1 RICRIWVIRCR 12

RESULT 38

AA91867
 ID AAY91867 standard; peptide; 12 AA.

XX AC AAY91867;

XX DT 06-JUN-2000 (first entry)

XX DE Amino acid sequence of cationic peptide REWH 53A5.

XX KW Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;
 KW leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma;
 KW breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
 KW multidrug resistance.

XX OS Synthetic.

XX PN WO9965506-A2.

XX PD 23-DEC-1999.

XX PF 14-JUN-1999; 99WO-CA000552.

XX PR 12-JUN-1998; 98US-00096541.

XX PA (MICR-) MICROLOGIX BIOTECH INC.

XX PI Friedland HD, Krieger TJ, Taylor R, Brfle D, Fraser JR, West MHP;

XX DR WPI; 2000-223549/19.

XX PT Novel pharmaceutical composition containing optionally activated
 PT polyoxyalkylene-modified cationic peptides, useful for treating tumors.

XX PS Disclosure; Page 16; 94pp; English.

XX CC This sequence represents a cationic peptide amino acid sequence, which
 CC can be used in the pharmaceutical composition of the invention. The
 CC invention relates to a pharmaceutical composition containing at least one
 CC activated polyoxyalkylene (APO)-modified cationic peptide. The
 CC modification of peptides with APO increases their activity against tumour
 CC cells, including those with a multidrug resistant phenotype. The
 CC pharmaceutical composition can be used to treat tumours, specifically
 CC lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary,
 CC cervix, uterus, skin, prostate, liver and colon

XX SQ Sequence 12 AA;

Query Match 71.0%; Score 44; DB 3; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RLCRIWVIRVCR 12
 |:|||||||
 Db 1 RLARIWVIRVAR 12

RESULT 39

AA91867
 ID AAY67331 standard; peptide; 12 AA.

XX AC AAY67331;

XX DT 11-APR-2000 (first entry)

XX DE Antimicrobial batenecicin peptide derivative BAC 2A-NH2.

XX KW Batenecicin; antimicrobial activity; cytostatic; antiproliferative;
 KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
 KW cell proliferative disorder; anticancer agent; BAC 2A-NH2.

XX OS Synthetic.

XX PN WO9960016-A2.

XX PD 25-NOV-1999.

XX PF 20-MAY-1999; 99WO-CA000414.

XX PR 20-MAY-1998; 98US-00082420.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PI Hancock REW, Wu M;

XX DR WPI; 2000-126379/11.

XX PT Antimicrobial peptide useful for inhibiting the growth of bacteria and as
 PT anticancer agents.

XX PS Claim 1; Page 36; 52pp; English.

XX CC This sequence represents a derivative of the bovine batenecicin peptide.
 CC Batenecicin is an antimicrobial cationic peptide, with antimicrobial
 CC activity. The invention relates to isolated antimicrobial peptides (see
 CC AAY67330-Y67347) derived from batenecicin, and includes analogues,
 CC derivatives, amidated variations and conservative variation. The peptides
 CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
 CC antifungal activities. The antimicrobial peptides are useful for
 CC inhibiting the growth of bacteria including both gram positive and
 CC negative species including *Escherichia coli*, *Pseudomonas aeruginosa* and
 CC *Salmonella typhimurium*. The peptides can be used to inhibit endotoxaemia
 CC or sepsis associated disorders, such as septic shock. The peptides can
 CC also be used to inhibit the growth of a eukaryotic cell, especially an
 CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
 CC can also be used to inhibit a cell proliferation-associated disorder

XX SQ Sequence 12 AA;

Query Match 71.0%; Score 44; DB 3; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RLCRIWVIRVCR 12
 |:|||||||
 Db 1 RLARIWVIRVAR 12

RESULT 40

ADA00619
 ID ADA00619 standard; peptide; 12 AA.

XX AC ADA00619;

XX XX

DT 06-NOV-2003 (first entry)
 DE Antimicrobial cationic peptide REWH 53A5.
 XX antimicrobial; cationic; viscosity-increasing agent; solvent; buffer;
 KW antibacterial; virucide; antiinflammatory; fungicide; protozoacide;
 KW parasiticide; vulnerary; dermatological; herbicide; insecticide;
 KW infection; systemic infection; sepsis; acne; disinfectant; herbicide;
 KW insecticide; silicone sealant.
 XX Synthetic.
 OS
 XX W02003015809-A2.
 PN
 XX 27-FEB-2003.
 PD
 XX 21-AUG-2002; 2002WO-US026525.
 PF
 XX 21-AUG-2001; 2001US-0314232P.
 PR
 XX 20-AUG-2002; 2002US-00225087.
 XX
 XX (MCCR-) MICROLOGIX BIOTECH INC.
 PA
 XX Krieger TJ, McNicol PJ, Frazer JR;
 PI
 XX WPI; 2003-332767/31.
 DR
 XX Composition containing stabilized antimicrobial cationic protein, useful
 PT for treating infections, particularly where associated with in-dwelling
 PT devices.
 PT
 XX Example 1; Page 50; 90pp; English.
 PS
 XX The present invention describes a composition (A) comprising an
 CC antimicrobial cationic peptide (I), a viscosity-increasing agent (II) and
 CC a solvent (III). Also described is a composition comprising (I), buffer
 CC (IV) and (III). (I) has antibacterial, virucide, antiinflammatory,
 CC fungicide, protozoacide, parasiticide, vulnerary, dermatological,
 CC herbicide and insecticide activities. (A) can be used to reduce the
 CC population of microflora (eukaryotes, prokaryotes or viruses) at a target
 CC site, particularly for treatment or prevention of infections. They can be
 CC used to treat a wide range of systemic infections (e.g. sepsis) and for
 CC topical treatment of wounds, but most especially can be used: (i) at
 CC sites where medical devices have been, or will be, inserted into the body
 CC (alternatively, they are used to treat the devices); and (ii) at sites on
 CC the skin (particularly for treating acne) or the mucosa. The devices
 CC treated are especially central venous, vascular dialysis, pulmonary
 CC artery, peritoneal dialysis or umbilical catheters. They may also be used
 CC as surface disinfectants; for treatment of clothing and air filters; in
 CC cosmetics and soaps; as herbicides and insecticides; in building
 CC materials (e.g. silicone sealants) and in processing animal products,
 CC e.g. hides. The present sequence represents an antimicrobial cationic
 CC peptide, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 12 AA;
 Query Match 71.0%; Score 44; DB 6; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RLCRIVVIRVCR 12
 || |||||
 Db 1 RLARIVVIRVAR 12

RESULT 41
 ABR63789
 ID ABR63789 standard; peptide; 12 AA.
 XX
 AC ABR63789;
 XX
 XX 15-OCT-2003 (first entry)
 DT
 .XX

DE Bovine cationic peptide bactericin Bac2A.
 XX
 KW Innate immunity effector; cationic peptide; sepsis; inflammation;
 KW microbial infection; antibacterial; antiinflammatory.
 XX
 OS Bos taurus.
 XX
 PN W02003049383-A2.
 XX
 XX 12-JUN-2003.
 PD
 XX 02-DEC-2002; 2002WO-CA001830.
 PF
 XX 03-DEC-2001; 2001US-0336632P.
 PR
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 XX Hancock REW, Finlay BB, Scott MG, Bowdish D, Rosenberger CM;
 PI Powers JS;
 PI
 XX WPI; 2003-513768/48.
 DR
 XX Identifying a polynucleotide regulated by one or more sepsis or
 XX inflammatory inducing agents and inhibited by a cationic peptide for
 PT blocking sepsis or inflammation by contacting the polynucleotide with the
 PT inducing agents.
 PT
 XX Example 2; Page 10; 203pp; English.
 PS
 XX The present invention relates to a method of identifying a polynucleotide
 CC or pattern of polynucleotides regulated by one or more sepsis or
 CC inflammatory inducing agents and inhibited by a cationic peptide, which
 CC comprises contacting the polynucleotide or polynucleotides with one or
 CC more sepsis or inflammatory inducing agents, contacting the
 CC polynucleotide or polynucleotides with a cationic peptide either
 CC simultaneously or immediately thereafter and determining a change in
 CC expression. The method is useful for identifying a polynucleotide or
 CC pattern of polynucleotides regulated by one or more sepsis or
 CC inflammatory inducing agents and inhibited by a cationic peptide for
 CC preparing a composition for preparing a composition for blocking sepsis
 CC or inflammation or for enhancing innate immunity. The present sequence is
 CC a cationic peptide shown in the exemplification of the invention
 XX
 SQ Sequence 12 AA;
 Query Match 71.0%; Score 44; DB 6; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RLCRIVVIRVCR 12
 || |||||
 Db 1 RLARIVVIRVAR 12

RESULT 42
 ADC98988
 ID ADC98988 standard; peptide; 12 AA.
 XX
 AC ADC98988;
 XX
 XX 01-JAN-2004 (first entry)
 DT
 XX Synthetic indolicidin analogue peptide - REWH 53A5.
 DE
 XX indolicidin analogue; antiseborrheic; dermatological; antiinflammatory;
 KW antiarthritic; immunosuppressive; vulnerary; antipruritic; antimicrobial;
 KW antipruritic; neuroprotective; antipsoriatic; inflammation; acne;
 KW arthritis; autoimmune disease; burn; Crohn's; colitis;
 KW contact hypersensitivity; delayed; eczema; endotoxin shock syndrome;
 KW fibromyositis; graft rejection; microbial infection; multiple sclerosis;
 KW parapsoriasis; psoriasis; sclerosis; seborrhea.
 XX
 XX Synthetic.

XX WO2003018619-A2.
 XX PD 06-MAR-2003.
 XX PF 26-AUG-2002; 2002WO-CA001351.
 XX PR 24-AUG-2001; 2001US-0315003P.
 XX PR 26-AUG-2002; 2002US-00229368.
 XX PA (MICR-) MICROLOGIX BIOTECH INC.
 XX PA (MCNI/) MCNICOL P J.
 XX PA (PAWL/) PAWLAK S K.
 XX PA (RUBI/) RUBINCHIK E.
 XX PA (CAME/) CAMERON D.
 XX PA (GUAR/) GUARNA M M.
 XX PI Mcnicol PJ, Pawlak SK, Rubinchik E, Cameron D, Guarna MM;
 XX WPI; 2003-393247/37.
 XX Novel indolicidin analog useful for treating or preventing inflammation
 PT at a target site associated with a condition such as acne, arthritis,
 PT burn, Crohn's disease, colitis, and in image analysis and diagnostic
 PT assays.
 XX Example 1; Page 49; 66pp; English.
 XX The invention relates to a novel indolicidin analogue. The analogue of
 CC the invention demonstrates antiseborrheic, dermatological,
 CC antiinflammatory, antiarthritic, immunosuppressive, vulnerary,
 CC antipruritic, antimicrobial, antipruritic, neuroprotective and
 CC antipsoriatic and may be useful for treating or preventing inflammation
 CC at a target site. The inflammation at the target site may be associated
 CC with a condition selected from acne, arthritis, autoimmune disease, burn,
 CC Crohn's disease, colitis, contact hypersensitivity, delayed
 CC hypersensitivity, eczema, endotoxin shock syndrome, fibromyositis, graft
 CC rejection, microbial infection, multiple sclerosis, parapsoriasis,
 CC psoriasis, sclerosis and seborrhea. The current sequence is that of the
 CC synthetic indolicidin analogue peptide of the invention.
 XX Sequence 12 AA;
 SQ
 Query Match 71.0%; Score 44; DB 7; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RLCRIWVIRVCR 12
 Db 1 RLARIWIRVAR 12
 RESULT 43
 ADY79756
 ID ADY79756 standard; peptide; 12 AA.
 AC ADY79756;
 XX 02-JUN-2005 (first entry)
 DT Amino acid sequence of bovine variant of bactenecin, Bac2A.
 DE immunostimulant; immunosuppressive; antinflammatory; innate immunity;
 XX cationic peptide; bacterial infection; sepsis; antibacterial; infection;
 KW immune stimulation; inflammation; synergistic therapy; bactenecin; Bac2A.
 XX Bos taurus.
 OS
 XX WO2005025607-A1.
 PN 24-MAR-2005.
 PD 10-SEP-2004; 2004WO-CA001602.

XX 12-SEP-2003; 2003US-00661471.
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 XX Hancock REW, Finlay BE, Scott MG, Bowdish D, Rosenberger CM;
 PI Powers JS;
 XX WPI; 2005-253849/26.
 XX Stimulating innate immunity used for inhibiting sepsis and inflammation
 PT comprises administering cationic peptide.
 XX Claim 1; SEQ ID NO 3; 238pp; English.
 CC The specification describes a method for stimulating innate immunity. The
 CC method comprises administering a cationic peptide. The innate immunity is
 CC evidenced by host immune cell activation, proliferation, differentiation
 CC or mitogen activated protein (MAP) kinase pathway activation. The method
 CC is used for stimulating innate immunity, for protecting against bacterial
 CC infection and regulating sepsis and inflammatory responses. The method
 CC provides synergistic therapy. The present sequence represents the bovine
 CC variant of bactenecin, Bac2A, a cationic peptide that is used in the
 CC method of the invention.
 XX Sequence 12 AA;
 SQ
 Query Match 71.0%; Score 44; DB 9; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RLCRIWVIRVCR 12
 Db 1 RLARIWIRVAR 12
 RESULT 44
 AAY67337
 ID AAY67337 standard; peptide; 12 AA.
 XX AAY67337;
 AC 11-APR-2000 (first entry)
 DT Antimicrobial bactenecin peptide derivative BAC 3K P.
 DE Bactenecin; antimicrobial activity; cytostatic; antiproliferative;
 KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
 KW cell proliferative disorder; anticancer agent; BAC 3K P.
 XX Synthetic.
 OS
 XX WO9960016-A2.
 PN 25-NOV-1999.
 PD 20-MAY-1999; 99WO-CA000414.
 PF 20-MAY-1998; 98US-00082420.
 PR (UYBR-) UNIV BRITISH COLUMBIA.
 PA Hancock REW, Wu M;
 XX WPI; 2000-126379/11.
 XX Antimicrobial peptide useful for inhibiting the growth of bacteria and as
 PT anticancer agents.
 XX Claim 1; Page 36; 52pp; English.
 PS This sequence represents a derivative of the bovine bactenecin peptide.
 CC Bactenecin is an antimicrobial cationic peptide, with antimicrobial

CC activity. The invention relates to isolated antimicrobial peptides (see
 CC AAY67330-Y67347) derived from bacterenecin, and includes analogues,
 CC derivatives, amidated variations and conservative variation. The peptides
 CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
 CC antifungal activities. The antimicrobial peptides are useful for
 CC inhibiting the growth of bacteria including both gram positive and
 CC negative species including *Escherichia coli*, *Pseudomonas aeruginosa* and
 CC *Salmonella typhimurium*. The peptides can be used to inhibit endotoxaemia
 CC or sepsis associated disorders, such as septic shock. The peptides can
 CC also be used to inhibit the growth of a eukaryotic cell, especially an
 CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
 CC can also be used to inhibit a cell proliferation-associated disorder

XX SQ Sequence 12 AA;

Query Match 69.4%; Score 43; DB 3; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.9;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
 Db 3 CPIVIVRVCK 12
 | | | | | | | |
 | | | | | | | |

RESULT 45
 AAY67333
 ID AAY67333 standard; peptide; 12 AA.

AC AAY67333;

DT 11-APR-2000 (first entry)

XX Antimicrobial bacterenecin peptide derivative BAC 2S-NH2.

Bacterenecin; antimicrobial activity; cytostatic; antiproliferative;
 KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
 KW cell proliferative disorder; anticancer agent; BAC 2S-NH2.

XX Synthetic.

XX WO9960016-A2.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-CA000414.

XX 20-MAY-1998; 98US-00082420.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Hancock RW, Wu M;

XX WPI; 2000-126379/11.

PT Antimicrobial peptide useful for inhibiting the growth of bacteria and as
 PT anticancer agents.

XX Claim 1; Page 36; 52pp; English.

XX This sequence represents a derivative of the bovine bacterenecin peptide.
 CC Bacterenecin is an antimicrobial cationic peptide, with antimicrobial
 CC activity. The invention relates to isolated antimicrobial peptides (see
 CC AAY67330-Y67347) derived from bacterenecin, and includes analogues,
 CC derivatives, amidated variations and conservative variation. The peptides
 CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
 CC antifungal activities. The antimicrobial peptides are useful for
 CC inhibiting the growth of bacteria including both gram positive and
 CC negative species including *Escherichia coli*, *Pseudomonas aeruginosa* and
 CC *Salmonella typhimurium*. The peptides can be used to inhibit endotoxaemia
 CC or sepsis associated disorders, such as septic shock. The peptides can
 CC also be used to inhibit the growth of a eukaryotic cell, especially an
 CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
 CC can also be used to inhibit a cell proliferation-associated disorder

XX SQ Sequence 12 AA;

Query Match 67.7%; Score 42; DB 3; Length 12;
 Best Local Similarity 83.3%; Pred. No. 4.2;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 12
 Db 1 RLSRIVVIRVS 12
 | | | | | | | |
 | | | | | | | |

RESULT 46

ABB81258

ID ABB81258 standard; peptide; 12 AA.

XX ABB81258;

DT 20-AUG-2002 (first entry)

XX Bac2S antibacterial peptide SEQ ID NO:25.

Antibacterial; glycopeptide; peptidic membrane associating element;
 KW bacterial infection; vancomycin; peptidoglycan biosynthesis inhibition;

XX Antibiotic.

XX Synthetic.

XX WO200236612-A1.

XX 10-MAY-2002.

XX 02-NOV-2001; 2001WO-GB004867.

XX 03-NOV-2000; 2000GB-00026924.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX (ADPR-) ADPROTECH LTD.

XX Cooper MA, Betley JR;

XX WPI; 2002-471498/50.

XX Antibacterial compound, useful for the treatment of a bacterial infection
 by e.g. gram positive or negative bacteria, comprises a conjugate of
 glycopeptide and peptidic membrane-associating element.

XX Disclosure; Page 21; 64pp; English.

XX The present invention describes an antibacterial compound (I), comprising
 CC a conjugates of glycopeptide and peptidic membrane-associating elements.
 CC (I) comprises the formula V-L-W-X, where: V = a glycopeptide moiety that
 CC inhibits peptidoglycan biosynthesis in bacteria; L = a linking group; W =
 CC a peptidic membrane-associating element; and X = H or a membrane-
 CC insertive element. Also described: (1) a method of treating or preventing
 CC a bacterial infection, comprising the administration of (I); and (2) use
 CC of (I) in the manufacture of a medicament for the treatment or prevention
 CC of a bacterial infection. (I) are used in the manufacture of a medicament
 CC for the treatment or prophylaxis of a bacterial infection in a human or
 CC animal body, including both the gram positive and gram negative bacteria
 CC including *Mycobacterium* sp., *Enterococcus* sp., *Escherichia* sp.,
 CC *Staphylococcus* sp., *Vibrio* sp., *Neisseria* sp., *Borrelia* sp., *Klebsiella*
 CC sp., *Hemophilus* sp., *Clostridium* sp., *Pseudomonas* sp., *Actinomyces* sp.,
 CC *Pneumococcus* sp. or *Salmonella* sp., particularly antibiotic resistant
 CC bacterial strains. (I) are also useful as wound treatment agents to
 CC prevent adhesion of bacteria to matrix proteins, especially fibronectin,
 CC exposed in wound tissue; and for prophylactic use in dental treatment as
 CC an alternative to, or in conjunction with, antibiotic prophylaxis. (I)
 CC has stronger binding to bacterial membranes which have a higher
 CC proportion of acidic phospholipids than the eukaryotic organisms, also
 CC having a higher proportion of membrane associated biosynthetic proteins.
 CC Vancomycin shows an enhanced antimicrobial activity upon derivatisation
 CC with (I) and is effective to treat the antibiotic resistant bacterial

CC strains. ABB81234 to ABB81272 represent peptides given in the
CC exemplification of the present invention
XX
SQ Sequence 12 AA;

Query Match 67.7%; Score 42; DB 5; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RLCRIWIRVCR 12
||| ||||| |
Db 1 RLSRIWIRVSR 12

RESULT 47
AAG25236
ID AAG25236 standard; protein; 304 AA.
XX
AC AAG25236;
XX XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29219.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 28-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.

Matches		6;	Conservative	4;	Mismatches	1;	Indels	0;	Gaps
QY	2	LCRIWIRVCR	12						
		: : :							
Db	69	VQVVSVRVC	79						
RESULT 48									
AAG46462									
ID	AAG46462 standard; protein; 618 AA.								
XX	AAG46462;								
XX	18-OCT-2000 (first entry)								
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 58456.								
XX	Protein identification; signal transduction pathway; metabolic pathway;								
XX	hybridisation assay; genetic mapping; gene expression control; promoter;								
XX	termination sequence.								
XX	Arabidopsis thaliana.								
XX	EP1033405-A2.								
XX	06-SEP-2000.								
XX	25-FEB-2000; 2000EP-00301439.								
XX	25-FEB-1999; 99US-0121825P.								
XX	05-MAR-1999; 99US-0123180P.								
XX	09-MAR-1999; 99US-0123548P.								
XX	23-MAR-1999; 99US-0125788P.								
XX	25-MAR-1999; 99US-0126264P.								
XX	29-MAR-1999; 99US-0126785P.								
XX	01-APR-1999; 99US-0127462P.								
XX	06-APR-1999; 99US-0128234P.								
XX	08-APR-1999; 99US-0128714P.								
XX	16-APR-1999; 99US-0129845P.								
XX	19-APR-1999; 99US-0130077P.								
XX	21-APR-1999; 99US-0130449P.								
XX	23-APR-1999; 99US-0130510P.								
XX	23-APR-1999; 99US-0130891P.								
XX	28-APR-1999; 99US-0131449P.								
XX	30-APR-1999; 99US-0132048P.								
XX	30-APR-1999; 99US-0132407P.								
XX	04-MAY-1999; 99US-0132484P.								
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XX	06-MAY-1999; 99US-0132487P.								
XX	07-MAY-1999; 99US-0132863P.								
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XX	14-MAY-1999; 99US-0134218P.								
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XX	14-MAY-1999; 99US-0134221P.								
XX	18-MAY-1999; 99US-0134768P.								
XX	19-MAY-1999; 99US-0134941P.								
XX	20-MAY-1999; 99US-0135124P.								
XX	21-MAY-1999; 99US-0135353P.								
XX	24-MAY-1999; 99US-0135629P.								
XX	25-MAY-1999; 99US-0136021P.								
XX	27-MAY-1999; 99US-0136392P.								
XX	28-MAY-1999; 99US-0136782P.								
XX	01-JUN-1999; 99US-0137222P.								
XX	03-JUN-1999; 99US-0137528P.								
XX	04-JUN-1999; 99US-0137502P.								
XX	07-JUN-1999; 99US-0137724P.								
XX	08-JUN-1999; 99US-0138094P.								
XX	10-JUN-1999; 99US-0138540P.								
XX	10-JUN-1999; 99US-0138847P.								
XX	14-JUN-1999; 99US-0139119P.								
XX	16-JUN-1999; 99US-0139452P.								

Query Match

Best Local Similarity

67.7%;

54.5%;

Score 42;

DB 3;

Length 304;

Pred. No. 88;

PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
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PR 23-AUG-1999; 99US-0149930P.
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PR 27-AUG-1999; 99US-0151065P.
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PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match Score 42; DB 3; Length 618;
Best Local Similarity 67.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LCRIWVRVCR 12
Db 69 VCQVSVRVC 79

RESULT 49
AAG46480
ID AAG46480 standard; protein; 662 AA.
XX AC AAG46480;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 58481.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX AC Arabidopsis thaliana.
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
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PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
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PR 24-JUN-1999; 99US-0140695P.
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PR 21-JUL-1999; 99US-0145086P.
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PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
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PR 08-OCT-1999; 99US-0158232P.
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PR 28-OCT-1999; 99US-0161920P.
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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 67.7%; Score 42; DB 3; Length 662;
Best Local Similarity 54.5%; Pred. NO. 1.8e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 12
:|:|:|:|:|
Db 69 VCQVSVRVC 79

RESULT 50
ADE25067
ID ADE25067 standard; protein; 662 AA.
XX AC ADE25067;
XX DT 29-JAN-2004 (first entry)

XX DE Plant growth associated protein seq id 42.
XX KW plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;
KW Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;
KW Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;
KW Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;
KW Quercus.
XX OS Magnoliophyta.
XX FN US2003188343-A1.
XX PD 02-OCT-2003.
XX PF 07-JAN-2003; 2003US-00338777.
XX PR 09-JAN-2002; 2002US-0347288P.
XX PA (LYNX-) LYNX THERAPEUTICS INC.
XX PI Bowen BA, Haudenschild CD, Buckler ES;
XX WPI; 2003-803305/75.
XX DR N-PSDB; ADE25037.
XX CC The invention describes an isolated or recombinant polypeptide (I) comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in the specification, or a conservative variant; (b) encoded by 1 of 30 sequences (S2), as given in the specification, or a conservative variant; (c) encoded by a sequence that hybridises under stringent conditions to S2; and (d) encoded by a sequence 70 % identical to S2. The expression or activity of (I) is modulated to modulate a plant growth trait in a flowering plant, of the family Brassicaceae, preferably in a plant that is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum, Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum, Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus, Pinus, or Quercus. A new method is used to detect genes for a plant growth trait. This is the amino acid sequence of plant growth associated protein.
XX SQ Sequence 662 AA;
Query Match 67.7%; Score 42; DB 7; Length 662;
Best Local Similarity 54.5%; Pred. NO. 1.8e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 12
:|:|:|:|:|
Db 69 VCQVSVRVC 79

RESULT 51
AAY67336
ID AAY67336 standard; peptide; 12 AA.

XX AC AAY67336;
XX DT 11-APR-2000 (first entry)

DE Antimicrobial bacterenecin peptide derivative BAC P, 2R-NH2.

XX KW Bactenecin; antimicrobial activity; cytostatic; antiproliferative;
XX antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
KW cell proliferative disorder; anticancer agent; BAC P 2R-NH2.
XX OS Synthetic.

XX W09960016-A2.
PN
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-CA000414.
XX
XX 20-MAY-1998; 98US-00082420.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Hancock REW, Wu M;
XX
XX WPI; 2000-126379/11.
DR
XX
XX Antimicrobial peptide useful for inhibiting the growth of bacteria and as
PT anticancer agents.
PT
XX
XX Claim 1; Page 36; 52pp; English.
PS
XX
CC This sequence represents a derivative of the bovine bactenecin peptide.
CC Bactenecin is an antimicrobial cationic peptide, with antimicrobial
CC activity. The invention relates to isolated antimicrobial peptides (see
CC AY67330-Y67347) derived from bactenecin, and includes analogues,
CC derivatives, amidated variations and conservative variation. The peptides
CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
CC antifungal activities. The antimicrobial peptides are useful for
CC inhibiting the growth of bacteria including both gram positive and
CC negative species including *Bacterichia coli*, *Pseudomonas aeruginosa* and
CC *Salmonella typhimurium*. The peptides can be used to inhibit endotoxaemia
CC or sepsis associated disorders, such as septic shock. The peptides can
CC also be used to inhibit the growth of a eukaryotic cell, especially an
CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
CC can also be used to inhibit a cell proliferation-associated disorder
XX
SQ Sequence 12 AA;

Query Match 66.1%; Score 41; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
||| | ||||
Db 1 RLCPRVRIRVCR 12

RESULT 52
ADM19746
ID ADM19746 standard; protein; 131 AA.
XX
AC ADM19746;
XX
XX 20-MAY-2004 (first entry)
XX
DE Protein encoded by novel human channel/transporter gene #64.
XX
XX immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
KW cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW gene therapy; channel/transporter protein; rheumatoid arthritis;
KW neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn; transplantation;
KW chemotaxis; food additive.
XX
OS Homo sapiens.
XX
XX W0200154472-A2.
PN
XX
XX
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001307.
PF

XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216847P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228524P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 23-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.

02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-02554097P.
PR 05-JAN-2001; 2001US-0259678P.
PR (HUMA-) HUMAN GENOME SCI INC.
PR Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-476159/51.
DR N-PSDB; ADM19267.
XX Isolated nucleic acid molecule encoding a channel/transporter protein is

used in preventing, treating or ameliorating a medical condition.
Claim 11; SEQ ID NO 553; 809pp; English.
The invention relates to an isolated nucleic acid molecule encoding a channel/transporter protein or sequences at least 95% identical to a these. The nucleic acids and proteins encoded by them are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a CC pathological condition. The antibodies to the proteins can also be used CC in alleviating symptoms associated with the disorders and in diagnostic CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac CC arrest, cerebrovascular disorders e.g. cerebral ischemia, angiodysplasia, CC nervous system disorders e.g. Alzheimer's disease, infections caused by CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection. CC The polypeptides can also be used to aid wound healing and epithelial CC cell proliferation, to prevent skin aging due to sunburn, to maintain CC organs before transplantation, for supporting cell culture of primary CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can CC also be used as a food additive or preservative to increase or decrease CC storage capabilities. This sequence corresponds to a protein of the CC invention.
XX Sequence 131 AA;
SQ

Query Match 66.1%; Score 41; DB 4; Length 131;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RLCRIVIRVC 11
Db 102 RLCRLVCLRHC 112
|||||:|
RESULT 53
AAV67339
ID AAY67339 standard; peptide: 14 AA.
XX AAV67339;
XX AAV67339;
DT 11-APR-2000 (first entry)
XX Antimicrobial bactericin peptide derivative BAC 3R, P, (V).
DE Antimicrobial bactericin peptide derivative BAC 3R, P, (V).
KW Bactenecin; antimicrobial activity; cytostatic; antiproliferative;
KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
KW cell proliferative disorder; anticancer agent; BAC 3R P V.
XX Synthetic.
OS WO9960016-A2.
PN 25-NOV-1999.
PD 20-MAY-1999; 99WO-CA000414.
PF 20-MAY-1998; 98US-00082420.
PR (UYBR-) UNIV BRITISH COLUMBIA.
PA Hancock REW, Wu M;
XX WPI; 2000-126379/11.
XX Antimicrobial peptide useful for inhibiting the growth of bacteria and as
XX anticancer agents.
XX Claim 1; Page 36; 52pp; English.

CC This sequence represents a derivative of the bovine bactenecin peptide.
 CC Bactenecin is an antimicrobial cationic peptide, with antimicrobial
 CC activity. The invention relates to isolated antimicrobial peptides (see
 CC AAY67330-Y67347) derived from bactenecin, and includes analogues,
 CC derivatives, amidated variations and conservative variation. The peptides
 CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
 CC antifungal activities. The antimicrobial peptides are useful for
 CC inhibiting the growth of bacteria including both gram positive and
 CC negative species including *Escherichia coli*, *Pseudomonas aeruginosa* and
 CC *Salmonella typhimurium*. The peptides can be used to inhibit endotoxaemia
 CC or sepsis associated disorders, such as septic shock. The peptides can
 CC also be used to inhibit the growth of a eukaryotic cell, especially an
 CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
 CC can also be used to inhibit a cell proliferation-associated disorder
 CC
 XX SQ Sequence 14 AA;

Query Match 65.3%; Score 40.5; DB 3; Length 14;
 Best Local Similarity 83.3%; Pred. No. 8.4;
 Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 RLCRIVVIRVCR 12
 Db 3 RLCPI-VIRVCR 13

RESULT 54
 ABM88679
 ID ABM88679 standard; protein; 447 AA.
 XX AC ABM88679;
 XX DT 02-JUN-2005 (first entry)
 XX DE Rice abiotic stress responsive polypeptide SEQ ID NO:6925.
 XX KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX OS Oryza sativa.
 XX PN W02003008540-A2.
 XX PD 30-JAN-2003.
 XX PF 21-JUN-2002; 2002WO-US019668.
 XX PR 22-JUN-2001; 2001US-0300112P.
 XX PR 24-AUG-2001; 2001US-0314662P.
 XX PR 26-SEP-2001; 2001US-0325277P.
 XX PR 21-NOV-2001; 2001US-0332132P.

(SYGN) SYNGENTA PARTICIPATIONS AG.

XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
 XX Moughamer T, Provart N, Rieke D, Zhu T;
 XX WPI; 2003-248011/24.
 XX
 XX New stress-responsive nucleic acid, useful for altering the
 XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 XX stress, salt stress or osmotic stress.
 XX
 XX Claim 1; SEQ ID NO 6925; 89pp; English.

CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or

CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX
 XX SQ Sequence 447 AA;

Query Match 62.9%; Score 39; DB 7; Length 447;
 Best Local Similarity 63.6%; Pred. No. 3.8e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 11
 Db 242 RLCRRVLVDVC 252

RESULT 55
 AAY67344
 ID AAY67344 standard; peptide; 13 AA.
 XX AC AAY67344;
 XX DT 11-APR-2000 (first entry)
 XX DE Antimicrobial bactenecin peptide derivative BAC R, P, W.
 XX KW Bactenecin; antimicrobial activity; cytostatic; antiproliferative;
 XX KW antiviral; antifungal; bacterial growth inhibitor; endotoxaemia; sepsis;
 XX KW cell proliferative disorder; anticancer agent; BAC R P W.
 XX OS Synthetic.
 XX PN W09960016-A2.
 XX PD 25-NOV-1999.
 XX PF 20-MAY-1999; 99WO-CA000414.
 XX PR 20-MAY-1998; 98US-00082420.
 XX PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX PI Hancock REW, Wu M;
 XX WPI; 2000-126379/11.
 XX Antimicrobial peptide useful for inhibiting the growth of bacteria and as
 XX anticancer agents.

Claim 1; Page 36; 52pp; English.

CC This sequence represents a derivative of the bovine bactenecin peptide.
 CC Bactenecin is an antimicrobial cationic peptide, with antimicrobial
 CC activity. The invention relates to isolated antimicrobial peptides (see
 CC AAY67330-Y67347) derived from bactenecin, and includes analogues,
 CC derivatives, amidated variations and conservative variation. The peptides
 CC have antimicrobial, cytostatic, antiproliferative, antiviral, and
 CC antifungal activities. The antimicrobial peptides are useful for
 CC inhibiting the growth of bacteria including both gram positive and
 CC negative species including *Escherichia coli*, *Pseudomonas aeruginosa* and
 CC *Salmonella typhimurium*. The peptides can be used to inhibit endotoxaemia
 CC or sepsis associated disorders, such as septic shock. The peptides can
 CC also be used to inhibit the growth of a eukaryotic cell, especially an
 CC animal, neoplastic cell, in particular a glioblastoma cell. The peptides
 CC can also be used to inhibit a cell proliferation-associated disorder
 CC
 XX SQ Sequence 13 AA;

Query Match 62.1%; Score 38.5; DB 3; Length 13;
 Best Local Similarity 76.9%; Pred. No. 16;
 Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 RLCRIV-VIRVCR 12
 DB 1 RRCPIVWIRVCR 13

RESULT 56
 ID ABO14090 standard; protein; 50 AA.
 AC ABO14090;
 XX 21-AUG-2003 (first entry)
 DT Novel human secreted protein #119.
 DE Human; secreted protein; cytostatic; neuroprotective; hepatotropic;
 KW gene therapy; cancer; liver disorder; hepatitis; neural disorder;
 KW Alzheimer's disease.
 OS Homo sapiens.
 XX US2003028003-A1.
 FN 06-FEB-2003.
 XX 12-OCT-2001; 2001US-00974879.
 PF 07-NOV-1997; 97US-0064900P.
 PR 07-NOV-1997; 97US-0064908P.
 PR 07-NOV-1997; 97US-0064911P.
 PR 07-NOV-1997; 97US-0064912P.
 PR 07-NOV-1997; 97US-0064983P.
 PR 07-NOV-1997; 97US-0064984P.
 PR 07-NOV-1997; 97US-0064985P.
 PR 07-NOV-1997; 97US-0064987P.
 PR 07-NOV-1997; 97US-0064988P.
 PR 07-NOV-1997; 97US-0066089P.
 PR 07-NOV-1997; 97US-0066090P.
 PR 07-NOV-1997; 97US-0066094P.
 PR 07-NOV-1997; 97US-0066095P.
 PR 07-NOV-1997; 97US-0066100P.
 PR 04-NOV-1998; 98WO-US023435.
 PR 05-MAY-1999; 99US-00305736.
 PR 13-OCT-2000; 2000US-0239893P.
 PR 28-MAR-2001; 2001US-00818683.
 XX (ROSE/) ROSEN C A.
 PA (FENG/) FENG P.
 PA (RUBE/) RUBEN S M.
 PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H S.
 PA (NIJJ/) NI J.
 PA (WEIY/) WEI Y.
 PA (SOPP/) SOPPET D R.
 PA (MOOR/) MOORE P A.
 PA (KYAW/) KYAW H.
 PA (LAPL/) LAPLEUR D W.
 PA (SHIY/) SHI Y.
 PA (JANA/) JANAT F.
 PA (ENDR/) ENDRESS G A.
 PA (CART/) CARTER K C.
 PA (BIRS/) BIRSE C E.
 XX Rosen CA, Feng P, Ruben SM, Ebner R, Olsen HS, Ni J, Wei Y;
 PI Soppet DR, Moore PA, Kyaw H, Lafleur DW, Shi Y, Janat F;
 PI Endress GA, Carter KC, Birse CE;
 XX WPI; 2003-479549/45.
 DR N-PSDB; ACD18977.
 XX New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g., cancer,
 PT liver disorders such as hepatitis or neural disorders such as Alzheimer's

PT disease.
 XX Claim 11; Page 395; 496pp; English.
 PS The invention describes a new isolated nucleic acid molecule comprising a
 CC sequence having at least 95% identity with a sequence comprising: (a) a
 CC polynucleotide (PN) fragment of a sequence comprising 420-3435 bp, or its
 CC allelic variant; (b) a PN fragment of the cDNA sequence; (c) a PN
 CC sequence encoding a polypeptide, or its fragment, domain, epitope or
 CC species homologue; or (d) a PN that hybridises under stringent conditions
 CC to any one of the sequences of (A)-(C). The nucleic acid is useful for
 CC preparing a medicament for preventing, treating or ameliorating a medical
 CC condition e.g., cancer, liver disorders such as hepatitis or neural
 CC disorders such as Alzheimer's disease. This is the amino acid sequence of
 CC a novel human secreted protein
 XX Sequence 50 AA;
 SQ Query Match 61.3%; Score 38; DB 6; Length 50;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVWIRVC 11
 DB 28 VCQVIVRVC 37

RESULT 57
 ID ADN60787 standard; protein; 50 AA.
 AC ADN60787;
 XX 01-JUL-2004 (first entry)
 DT Human secreted polypeptide #119.
 DE Human; secreted polypeptide; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; breast; liver;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; nervous system disorder; Alzheimer's disease;
 KW bacterial infection; viral infection; fungal infection; ocular disorder;
 KW corneal infection; wound healing; epithelial cell proliferation;
 KW skin aging; sunburn; organ transplantation; tissue regeneration;
 KW chemotaxis; food additive; food preservative; fat content; vitamin;
 KW mineral.
 XX Homo sapiens.
 OS US2004038277-A1.
 PN 26-FEB-2004.
 XX 18-JUL-2003; 2003US-00621401.
 PF 07-NOV-1997; 97US-0064900P.
 PR 07-NOV-1997; 97US-0064908P.
 PR 07-NOV-1997; 97US-0064911P.
 PR 07-NOV-1997; 97US-0064912P.
 PR 07-NOV-1997; 97US-0064983P.
 PR 07-NOV-1997; 97US-0064984P.
 PR 07-NOV-1997; 97US-0064985P.
 PR 07-NOV-1997; 97US-0064987P.
 PR 07-NOV-1997; 97US-0064988P.
 PR 07-NOV-1997; 97US-0066089P.
 PR 07-NOV-1997; 97US-0066090P.
 PR 07-NOV-1997; 97US-0066094P.
 PR 07-NOV-1997; 97US-0066095P.
 PR 07-NOV-1997; 97US-0066100P.
 PR 04-NOV-1998; 98WO-US023435.
 PR 05-MAY-1999; 99US-00305736.
 PR 13-OCT-2000; 2000US-0239893P.
 PR 28-MAR-2001; 2001US-00818683.

KW bacterial infection; viral infection; parasitic infection; osteoporosis;
 KW wound; atherosclerosis; Alzheimer's disease; Parkinson's disease; ulcer;
 KW food additive; food preservative.

XX Homo sapiens.

XX US2003211472-A1.

XX 13-NOV-2003.

XX 28-MAR-2001; 2001US-00818683.

XX 05-MAY-1999; 99US-00305736.

XX (FENG/) FENG P.

XX (RUBE/) RUBEN S M.

XX (ROSE/) ROSEN C A.

XX (EBNE/) EBNER R.

XX (OLSE/) OLSEN H S.

XX (NIJ/) NI J.

XX (WEI/) WEI Y.

XX (SOPP/) SOPPET D R.

XX (MOOR/) MOORE P A.

XX (KYAW/) KYAW H.

XX (LAF/) LAFLEUR D W.

XX (SHI/) SHI Y.

XX (JANA/) JANAT F.

XX (ENDR/) ENDRESS G A.

XX (CART/) CARTER K C.

XX Feng P, Ruben SM, Rosen CA, Ebner R, Olsen HS, Ni J, Wei Y;

PI Soppet DR, Moore PA, Kyaw H, Lafleur DW, Shi Y, Janat F;

PI Endress GA, Carter KC;

XX WPI; 2004-051575/05.

DR N-PSDB; ADG78368.

XX New secreted nucleic acid for diagnosing, preventing or treating diseases
 PT associated with aberrant expression or activity of the polypeptide it
 PT encodes, e.g. cancer, human immunodeficiency virus, Parkinson's disease,
 PT or diabetes.

XX Claim 11; SEQ ID NO 257; 377pp; English.

XX The invention also relates to human secreted proteins and the nucleic
 CC acids encoding them. The proteins and nucleic acids are useful in
 CC diagnosing, preventing, prognosing or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the secreted
 CC proteins, such as immune disorders, haematopoietic disorders,
 CC hyperproliferative disorders, infectious diseases or inflammatory
 CC disorders. In particular, the diseases or disorders are HIV, anaemia,
 CC thrombocytopenia, bleeding, stroke, myocardial infarction, Addison's
 CC disease, rheumatoid arthritis, dermatitis, Grave's disease, multiple
 CC sclerosis, glomerulonephritis, diabetes, graft-versus-host disease,
 CC inflammatory bowel disease, cancer, bacterial infections, viral
 CC infections, parasitic infections, osteoporosis, wounds, atherosclerosis,
 CC Alzheimer's disease, Parkinson's disease or ulcers. The sequences may
 CC also be used as food additives or preservatives, or for modulating
 CC mammalian mental or physical characteristics. The nucleic acids are also
 CC used in chromosome mapping, in forensic biology or as molecular weight
 CC markers. This sequence represents a human secreted protein of the
 CC invention.

XX Sequence 51 AA;

Query Match 61.3%; Score 38; DB 8; Length 51;

Best Local Similarity 50.0%; Pred. No. 71;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIWVIRVC 11

Db 28 VQYVIRVC 37

RESULT 60

AAU65577

ID AAU65577 standard; protein; 58 AA.

XX AC AAU65577;

XX 27-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein #26473.

XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

XX KW dermatological; osteopathic; neuroprotectant.

XX OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US012865.

XX PR 21-APR-2000; 2000US-0199047P.

XX PR 02-JUN-2000; 2000US-0208841P.

XX PR 07-JUL-2000; 2000US-0216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

DR N-PSDB; AAS59677.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX Example 1; SEQ ID NO 26772; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

CC polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by

CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for

CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 58 AA;

XX Query Match 61.3%; Score 38; DB 4; Length 58;

Best Local Similarity 60.0%; Pred. No. 80;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIWVIRVC 11

Db 45 VCCLVVRVC 54

RESULT 61
ID ABM62096 standard; protein; 58 AA.
XX
AC ABM62096;
XX
DT 20-OCT-2003 (first entry)
XX
DE Propionibacterium acnes predicted ORF-encoded polypeptide #26772.
XX
KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN W02003033515-A1.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallie-Douglas J;
XX
DR WPI; 2003-381789/36.
DR N-PSDB; ACF64606.
XX
PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.
XX
PS Example 1; SEQ ID NO 26772; 1481pp; English.
XX
CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM5624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 58 AA;
Query Match 61.3%; Score 38; DB 6; Length 58;
Best Local Similarity 60.0%; Pred. No. 80;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIWIRVC 11
Db :|:|:|
45 VCCLVVRVC 54
RESULT 62
AAU45256
ID AAU45256 standard; protein; 71 AA.
XX
AC AAU45256;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #6152.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN W0200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59525.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 6451; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

Sequence 71 AA;
Query Match 61.3%; Score 38; DB 4; Length 71;
Best Local Similarity 58.3%; Pred. No. 97;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIWIRVCR 12
 ||| |::|||
 Db 45 RRCRGVLLRCCR 56

RESULT 63
 ID ABM41775
 XX ABM41775 standard; protein; 71 AA.

AC ABM41775;

XX 20-OCT-2003 (first entry)

DE Propionibacterium acnes predicted ORF-encoded polypeptide #6451.

XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;

XX immunostimulant; immune response; vaccine.

OS Propionibacterium acnes.

XX WO2003033515-A1.

XX 24-APR-2003.

XX 11-OCT-2002; 2002WO-US032727.

XX 15-OCT-2001; 2001US-00978825.

XX (CORI-) CORIXA CORP.

XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;

PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

PI Barth B, Vallieue-Douglas J;

XX WPI; 2003-381789/36.

XX N-PSDB; ACF64454.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the

PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,

PT or for stimulating an immune response specific for a P. acnes protein.

XX Example 1; SEQ ID NO 6451; 1481bp; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

CC encoding a Propionibacterium acnes protein. The invention also relates to

CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to

CC immunogenic fragments of P. acnes polypeptides. The invention

CC additionally encompasses expression vectors and host cells comprising a

CC polynucleotide of the invention; antibodies against polypeptides of the

CC invention; fusion proteins comprising a polypeptide of the invention; a

CC method for stimulating an immune response specific for a P. acnes

CC polypeptide and an isolated T cell population comprising T cells prepared

CC via this method; a vaccine composition (comprising P. acnes polypeptides,

CC polynucleotides, antibodies, fusion proteins, T cell populations, or

CC antigen-presenting cells that express the polypeptide); a method and kit

CC for detecting or determining the presence or absence of P. acnes in a

CC patient; and a method for inhibiting the development of P. acnes in a

CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion

Query Match 61.3%; Score 38; DB 6; Length 71;
 Best Local Similarity 58.3%; Pred. No. 97;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIWIRVCR 12
 ||| |::|||
 Db 45 RRCRGVLLRCCR 56

RESULT 64
 ADM98644

ID ADM98644 standard; protein; 343 AA.

XX AC ADM98644;

XX 01-JUL-2004 (first entry)

DE Geranylgeranyl pyrophosphate synthase polypeptide #43.

XX Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor;

KW diterpene synthase; defence toxin; volatile defensive signal;

XX pollinator attractant; photoprotectant; enzyme.

OS Arabidopsis thaliana.

XX US2004072323-A1.

XX 15-APR-2004.

XX 07-JAN-2002; 2002US-00041018.

XX 05-JAN-2001; 2001US-0259880P.

XX (MATS/) MATSUDA S P T.

XX (HART/) HART E A.

XX Matsuda SPT, Hart EA;

XX WPI; 2004-373921/35.

XX New unicellular organisms comprising exogenous nucleic acids encoding a

PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for

PT producing diterpenes and diterpene precursors.

XX Claim 30; SEQ ID NO 64; 38pp; English.

XX The invention relates to a unicellular organism for producing a diterpene

CC or diterpene precursor comprising an exogenous nucleic acid sequence

CC encoding a geranylgeranyl pyrophosphate synthase under the control of a

CC promoter operable in the organism, and an exogenous nucleic acid sequence

CC encoding a diterpene synthase under the control of a promoter operable in

CC the organism. The invention also relates to methods of producing a

CC diterpene or diterpene precursor and a method of isolating a diterpene

CC synthase comprising growing several cells in the presence of a

CC polyaromatic resin to make a cell/resin mixture, where at least one of

CC the cells further comprises at least one isolated and purified nucleic

CC acid sequence of a yeast expression library, and the expression of the

CC nucleic acid sequence is regulated by an inducible promoter under

CC conditions where the expression is induced, filtering the cell/resin

CC mixture, extracting the cell/resin mixture with alcohol to produce an

CC organic eluent and analysing the organic eluent by a screening method

CC including chromatography and/or spectroscopy, to identify the nucleic

CC acid sequence encoding the diterpene synthase. The unicellular

CC microorganism is useful as a diterpene or diterpene precursor producing

CC system. Diterpenes, in plants, serve as defence toxins, volatile

CC defensive signals, pollinator attractants and photoprotectants. This

CC sequence represents a geranylgeranyl pyrophosphate synthase polypeptide

CC of the invention. Note: The sequence data for this patent did not form

CC part of the printed specification but was obtained in electronic format

CC from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 343 AA;

XX

Query Match 61.3%; Score 38; DB 8; Length 343;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVIRVC 11
|||:|:|
Db 2 LCKIINRPC 11

RESULT 65

ADM98612
ID ADM98612 standard; protein; 343 AA.

XX
AC ADM98612;

XX
DT 01-JUL-2004 (first entry)

XX Geranylgeranyl pyrophosphate synthase polypeptide #11.

XX Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor;
KW diterpene synthase; defence toxin; volatile defensive signal;
KW pollinator attractant; photoprotectant; enzyme.

XX Arabidopsis thaliana.

XX US2004072323-A1.

XX
PN 15-APR-2004.

XX
PD 07-JAN-2002; 2002US-00041018.

XX
PF 05-JAN-2001; 2001US-0259880P.

XX (MATS/) MATSUDA S P T.

XX (HART/) HART E A.

XX Matsuda SPT, Hart EA;

XX WPI; 2004-373921/35.

XX New unicellular organisms comprising exogenous nucleic acids encoding a
PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for
PT producing diterpenes and diterpene precursors.

XX Claim 30; SEQ ID NO 32; 38pp; English.

XX The invention relates to a unicellular organism for producing a diterpene
CC or diterpene precursor comprising an exogenous nucleic acid sequence
CC encoding a geranylgeranyl pyrophosphate synthase under the control of a
CC promoter operable in the organism, and an exogenous nucleic acid sequence
CC encoding a diterpene synthase under the control of a promoter operable in
CC the organism. The invention also relates to methods of producing a
CC diterpene or diterpene precursor and a method of isolating a diterpene
CC synthase comprising growing several cells in the presence of a
CC polyaromatic resin to make a cell/resin mixture, where at least one of
CC the cells further comprises at least one isolated and purified nucleic
CC acid sequence of a yeast expression library, and the expression of the
CC nucleic acid sequence is regulated by an inducible promoter under
CC conditions where the expression is induced, filtering the cell/resin
CC mixture, extracting the cell/resin mixture with alcohol to produce an
CC organic eluent and analysing the organic eluent by a screening method
CC including chromatography and/or spectroscopy, to identify the nucleic
CC acid sequence encoding the diterpene synthase. The unicellular
CC microorganism is useful as a diterpene or diterpene precursor producing
CC system. Diterpenes, in plants, serve as defence toxins, volatile
CC defensive signals, pollinator attractants and photoprotectants. This
CC sequence represents a geranylgeranyl pyrophosphate synthase polypeptide
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification but was obtained in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 343 AA;

SQ Sequence 60 AA;

Query Match 61.2%; Score 38; DB 8; Length 343;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVIRVC 11
|||:|:|
Db 2 LCKIINRPC 11

RESULT 66

AAU58705
ID AAU58705 standard; protein; 60 AA.

XX
AC AAU58705;

XX
DT 13-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #19601.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX
PN 01-NOV-2001.

XX
PD 20-APR-2001; 2001WO-US012865.

XX
PF 21-APR-2000; 2000US-0199047P.

XX
PR 02-JUN-2000; 2000US-0208841P.

XX
PR 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59594.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX Example 1; SEQ ID NO 19900; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,thalmitis.
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 60 AA;

Query Match 59.7%; Score 37; DB 4; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVWVRC 11
Db 19 CRRMVVRVC 27

RESULT 67
ABM5224
ID ABM5224 standard; protein; 60 AA.

XX AC ABM5224;

XX DT 20-OCT-2003 (first entry)

XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #19900.

XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX KW immunoestimulant; immune response; vaccine.

XX OS Propionibacterium acnes.

XX PN WO2003033515-A1.

XX PD 24-APR-2003.

XX PF 11-OCT-2002; 2002WO-US032727.

XX PR 15-OCT-2001; 2001US-00978825.

XX PA (CORI-) CORIYA CORP.

XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barth B, Vallieue-Douglas J;

XX DR WPI; 2003-381789/36.
XX DR N-PSDB; ACF64523.

XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX PT or for stimulating an immune response specific for a P. acnes protein.

XX PS Example 1; SEQ ID NO 19900; 1481pp; English.

XX CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX CC encoding a Propionibacterium acnes protein. The invention also relates to
XX CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX CC immunogenic fragments of P. acnes polypeptides. The invention
XX CC additionally encompasses expression vectors and host cells comprising a
XX CC polynucleotide of the invention; antibodies against polypeptides of the
XX CC invention; fusion proteins comprising a polypeptide of the invention; a
XX CC method for stimulating an immune response specific for a P. acnes
XX CC polypeptide and an isolated T cell population comprising T cells prepared
XX CC via this method; a vaccine composition (comprising P. acnes polypeptides,
XX CC polynucleotides, antibodies, fusion proteins, T cell populations, or
XX CC antigen-presenting cells that express the polypeptide); a method and kit
XX CC for detecting or determining the presence or absence of P. acnes in a
XX CC patient; and a method for inhibiting the development of P. acnes in a
XX CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX CC proteins, T cell populations or antigen-presenting cells that express the
XX CC polypeptides are useful for diagnosing, preventing or treating acne
XX CC vulgaris, or for stimulating an immune response specific for a P. acnes
XX CC protein. The polynucleotides can also be used as probes or primers for
XX CC nucleic acid hybridisation. The vaccine composition is useful for the
XX CC stimulation of an immune response against P. acnes, or for treating acne,
XX CC and the kit is useful for performing a diagnostic assay. The present
XX CC sequence represents a polypeptide predicted to be encoded by an ORF (open
XX CC reading frame) contained within the P. acnes polynucleotides of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 60 AA;

Query Match 59.7%; Score 37; DB 6; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVWVRC 11
Db 19 CRRMVVRVC 27

RESULT 68
ABO81457
ID ABO81457 standard; protein; 181 AA.

XX AC ABO81457;

XX DT 29-JUL-2004 (first entry)

XX DE Pseudomonas aeruginosa polypeptide #13632.

XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX PN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094190P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX DR WPI; 2003-615309/58.
XX DR N-PSDB; ABD15028.

XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.

XX PS Disclosure; SEQ ID NO 30203; 455pp; English.

XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,
XX CC for the ability to bind a P. aeruginosa nucleic acid, as components of
XX CC effective antibacterial targets, as targets for antibacterial drugs,
XX CC including anti-P. aeruginosa drugs, as templates for recombinant
XX CC production of P. aeruginosa-derived peptides or polypeptides, as target
XX CC components for diagnosis and/or treatment of P. aeruginosa-caused
XX CC infection, and in detection of P. aeruginosa sequences or other sequences
XX CC of Pseudomonas species using biochip technology. Sequences ABO67826-
XX CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format from USPTO at
XX CC seqdata.uspto.gov/sequence.html

XX CC Sequence 181 AA;

Query Match 59.7%; Score 37; DB 7; Length 181;
Best Local Similarity 63.6%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVWVRC 12


```

Db      137 LCRRSVRSCR 147
|||||:|:|
RESULT 69
ABB64054
ID ABB64054 standard; protein; 378 AA.
XX
XX ABB64054;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 18954.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
KW
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US009231.
PF
XX
XX 23-MAR-2000; 2000US-0191637P.
PR
XX
XX 11-JUL-2000; 2000US-00614150.
PR
XX
XX (PEKE ) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI; 2001-656860/75.
DR
XX
XX N-PSDB; ABL08157.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
PT
XX
XX Disclosure; SEQ ID NO 18954; 21pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 378 AA;
SQ
Query Match 59.7%; Score 37; DB 4; Length 378;
Best Local Similarity 58.3%; Pred. No. 6.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVCR 12
|      |:|:|:|
Db      49 REARVFLIRVCR 60

RESULT 70
AAB59829
ID AAB59829 standard; protein; 1618 AA.
XX
XX AAB59829;
AC
XX
XX 11-SEP-2003 (revised)
DT
XX
XX 04-APR-2001 (first entry)
DT
XX
XX Protein #6 encoded by TutsD/E gene.
DE

```

```

XX
KW Toluene degradation; enzyme; waste degradation; TutsE; TutsD.
XX
OS Thauera aromatica.
OS Stenotrophomonas maltophilia.
OS Geobacter metallireducens.
OS Azarcus tolulyticus.
XX
XX WO200072650-A2.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 24-MAY-2000; 2000WO-US014298.
PF
XX
XX 01-JUN-1999; 99US-00323872.
PR
XX
XX (UYOH-) UNIV OHIO.
PA
XX
XX Coschigano PW;
PI
XX
XX WPI; 2001-041080/05.
DR
XX
XX N-PSDB; AAF23627.
DR
XX
XX Composition comprising toluene degrading enzyme useful for biological
PT treatment of organic compounds, especially for degrading toluene or its
PT analogs.
PT
XX
XX Disclosure; Fig 12; 122pp; English.
PS
XX
XX The present invention relates to toluene degrading enzyme genes and
CC proteins tutH (see AAF23629 and AAB59831), tutI (AAF23630 and AAB59832),
CC tutF (AAF23631 and AAB59833) and tutG (AAF23632 and AAB59834). The
CC toluene degrading enzymes are homologues of pyruvate formate lyase. The
CC toluene degrading enzymes are useful for biological treatment of organic
CC compounds and in particular for the degradation of toluene and its
CC analogs contained in liquid or solid waste source. The present sequence
CC is a protein sequence encoded by toluene degrading enzyme gene, TutsD/E.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 1618 AA;
SQ
Query Match 59.7%; Score 37; DB 4; Length 1618;
Best Local Similarity 45.5%; Pred. No. 2.6e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVCR 11
|      |:|:|:|
Db      298 RMCALALIRMC 308

RESULT 71
AAE35490
ID AAE35490 standard; protein; 1953 AA.
XX
XX AAE35490;
AC
XX
XX 17-JUN-2003 (first entry)
DT
XX
XX Streptomyces platensis subspecies rosaceus dorrigin ORF7 protein.
DE
XX
XX Polyketide biosynthesis; dorrigin; DORR; lactimidomycin; LACT.
KW
XX
XX Streptomyces platensis.
OS
XX
XX Key Location/Qualifiers
FH Domain 62..124
FT /note= "Acyl carrier protein (ACP) 9 domain"
FT Domain 175..612
FT /note= "Ketosynthase (KS) 10 domain"
FT Domain 622..777
FT /note= "Interaction domain 10"
FT Domain 793..1061
FT /note= "Dehydratase (DH) 10 domain"
FT

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PD 18-DEC-2003.
 XX 08-NOV-2002; 2002US-00291265.
 PF
 XX 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-00663870.
 PR 25-JAN-2001; 2001US-0002623.
 PR 03-AUG-2001; 2001US-00922279.
 XX
 PA (TANG/) TANG Y T.
 PA (LIUC/) LIU C.
 PA (ASUN/) ASUNDI V.
 PA (CHEN/) CHEN R.
 PA (QIAN/) QIAN X B.
 PA (WANG/) WANG Z W.
 PA (WEHR/) WEHRMAN T.
 PA (ZHAN/) ZHANG J.
 PA (ZHOU/) ZHOU P.
 PA (CAO/) CAO Y.
 PA (DRMA/) DRMANAC R T.
 XX
 XX Tang YT, Liu C, Asundi V, Chen R, Qian XB, Wang ZW, Wehrman T;
 PI Zhang J, Zhou P, Cao Y, Drmanac RT;
 XX
 DR WPI; 2004-061257/06.
 XX
 XX New polynucleotides and polypeptides useful for diagnosing, preventing or
 PT treating diseases involving aberrant protein expression or activity, e.g.
 PT hemophilia, wounds, stroke, thrombosis, cancer or autoimmune disorders.
 XX
 XX Claim 20; SEQ ID NO 757; 85pp; English.
 PS
 XX The invention relates to new isolated polynucleotides and polypeptides.
 CC The sequences, compositions and methods of the invention are useful for
 CC diagnosing, preventing or treating diseases involving aberrant protein
 CC expression or biological activity, such as coagulation disorders (e.g.
 CC haemophilia), wounds, stroke, thrombosis, myocardial infarction, cancer,
 CC bone fractures, Alzheimer's disease, Parkinson's disease and autoimmune
 CC disorders. The polynucleotides may be used as hybridisation probes, as
 CC oligomers or primers, for polymerase chain reaction, for chromosome and
 CC gene mapping, in the recombinant production of proteins and in generation
 CC of antisense DNA or RNA. The polypeptides may be used in generating
 CC antibodies, as molecular weight markers or as food supplements. This
 CC sequence represents a human polypeptide of the invention.
 XX
 SQ Sequence 47 AA;
 Query Match 58.1%; Score 36; DB 8; Length 47;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 LCRIWIRVC 11
 ||| | | | | |
 Db 6 LCSICVRLC 15
 RESULT 76
 AAU47375
 ID AAU47375 standard; protein; 65 AA.
 XX
 AC AAU47375;
 XX
 XX 27-FEB-2002 (first entry)
 DT
 XX
 DE Propionibacterium acnes immunogenic protein #8271.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX

OS Propionibacterium acnes.
 XX WO200181581-A2.
 PN
 XX 01-NOV-2001.
 PD
 XX 20-APR-2001; 2001WO-US012865.
 PF
 XX 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 XX WPI; 2001-616774/71.
 DR N-PSDB; AAS59538.
 DR
 XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 PT
 XX Example 1; SEQ ID NO 8570; 1069pp; English.
 PS
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 65 AA;
 Query Match 58.1%; Score 36; DB 4; Length 65;
 Best Local Similarity 77.8%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RLRCRVIR 9
 ||| | | | | |
 Db 1 RLRCRVVR 9
 RESULT 77
 ABM43894
 ID ABM43894 standard; protein; 65 AA.
 XX
 AC ABM43894;
 XX
 XX 20-OCT-2003 (first entry)
 DT
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #8570.
 XX
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX
 XX Propionibacterium acnes.
 OS

PA (HANZ/) HANZEL D K.
 XX Penn SG, Rank DR, Hanzel DK;
 XX WPI; 2004-119264/12.
 XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX
 XX Claim 45; SEQ ID NO 29110; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX
 XX Sequence 75 AA;
 SQ
 Query Match 58.1%; Score 36; DB 8; Length 75;
 Best Local Similarity 60.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LCRIVVIRVC 11
 |||:|:|
 Db 19 LCRLLVHLVC 28
 RESULT 80
 ABG14129
 ID ABG14129 standard; protein; 115 AA.
 XX
 XX ABG14129;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #14120.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX

OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 PF
 XX 31-MAR-2000; 2000US-00540217.
 PR
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR
 DR N-PSDB; AAS78316.
 XX
 CC New isolated polynucleotide and encoded polypeptides, useful in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits and to assess
 CC biodiversity.
 PT
 PT Claim 20; SEQ ID NO 44488; 103pp; English.
 XX
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 115 AA;
 SQ
 Query Match 58.1%; Score 36; DB 4; Length 115;
 Best Local Similarity 58.3%; Pred. No. 3.2e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LCRIVVIRVC 12
 |||:|:|
 Db 101 RRCILAHPCR 112
 RESULT 81
 ADC87319
 ID ADC87319 standard; protein; 269 AA.
 XX
 XX ADC87319;
 AC
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human GPCR protein SEQ ID NO:1772.
 XX
 KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX

PN EPI270724-A2.
 XX
 PD 02-JAN-2003.
 XX
 PF 18-JUN-2002; 2002EP-00013517.
 XX
 PR 18-JUN-2001; 2001JP-00246789.
 XX
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX
 DR WPI; 2003-315783/31.
 DR N-PSDB; ADC87318.
 XX
 XX New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 XX
 PS Claim 2; SEQ ID NO 1772; 28pp; English.
 XX
 CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The protein
 CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
 XX
 SQ Sequence 269 AA;
 Query Match 58.1%; Score 36; DB 7; Length 269;
 Best Local Similarity 54.5%; Pred. No. 7e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RLCRIIVIRVC 11
 Db 91 RVCVFYIRVC 101
 RESULT 82
 ADX68272
 ID ADX68272 standard; protein; 284 AA.
 XX
 AC ADX68272;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 39115.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.
 XX
 XX US2004034888-A1.
 PN
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 XX 06-MAY-1999; 99US-00304517.
 PR
 PR 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABR/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.
 XX
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 39115; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 284 AA;
 Query Match 58.1%; Score 36; DB 8; Length 284;
 Best Local Similarity 54.5%; Pred. No. 7.4e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RLCRIIVIRVC 11
 Db 187 RACRVNPLRVC 197
 RESULT 83
 ADC95320
 ID ADC95320 standard; protein; 334 AA.
 XX
 AC ADC95320;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE E. faecium protein sequence SEQ ID 4947.
 XX
 KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KW abdominal-pelvic infection.
 KW
 XX Enterococcus faecium.
 OS
 XX US6583275-B1.
 PN
 XX
 PD 24-JUN-2003.
 XX
 PF 30-JUN-1998; 98US-00107532.
 XX
 XX 02-JUL-1997; 97US-0051571P.
 PR
 PR 14-MAY-1998; 98US-0085598P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA
 XX Doucette-Stamm LA, Bush D;
 PI

XX WPI; 2003-799836/75.
DR N-PsDB; ADC91666.
XX
PT New isolated nucleic acid derived from *Enterococcus faecium* encoding an
PT *Enterococcus faecium* polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX
XX Example 1; SEQ ID NO 4947; 243pp; English.
XX
XX The invention relates to an isolated nucleic acid derived from
CC *Enterococcus faecium* encoding an *Enterococcus faecium* polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids are useful for diagnosing pathological conditions
CC resulting from *E. faecium* bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating *Enterococcus faecium* infections. The present sequence represents
CC one if the disclosed *E. faecium* proteins.
XX
XX Sequence 334 AA;
SQ
Query Match 58.1%; Score 36; DB 7; Length 334;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RLCRIWVIRVC 12
Db 1 RLCRIIRKVC 12
|||:|:|:|:
|||:|:|:|:
RESULT 84
ADS43623
ID ADS43623 standard; protein; 391 AA.
XX
XX ADS43623;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Bacterial polypeptide #22053.
DE
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
XX Bacteria.
OS
XX
XX US2003233675-A1.
FN
XX
XX 18-DEC-2003.
PD
XX
XX 20-FEB-2003; 2003US-00369493.
PF
XX
XX 21-FEB-2002; 2002US-0360039P.
PR
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
PT
XX
XX Claim 1; SEQ ID NO 22053; 122pp; English.
PS
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 391 AA;
SQ
Query Match 58.1%; Score 36; DB 8; Length 391;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LCRIVWIRVC 11
Db 327 LCQIVLYKIC 336
|||:|:|:|:
|||:|:|:|:
RESULT 85
ADK41695
ID ADK41695 standard; protein; 462 AA.
XX
XX ADK41695;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Maize amino acid transporter protein.
DE
XX
XX amino acid transporter; plant; animal nutrition.
KW
XX
XX Zea mays.
OS
XX
XX WO2003066879-A2.
FN
XX
XX 14-AUG-2003.
PD
XX
XX 31-JAN-2003; 2003WO-US002978.
PF
XX
XX 01-FEB-2002; 2002US-0353062P.
PR
XX
XX 31-JAN-2003; 2003US-00355430.
PR
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
PA

PI Dong J;
 XX WPI; 2003-731505/69.
 DR N-PSDB; ADK41696.
 XX
 CC New nucleic acid molecules encoding amino acid transporters, useful for
 PT altering the activity of the amino acid transporters in a plant, or for
 PT producing a plant tissue with an increased amino acid content.
 XX
 PS Claim 8; SEQ ID NO 14; 192pp; English.
 XX
 CC The invention relates to a purified nucleic acid molecule encoding an
 CC amino acid transporter protein, a sequence having at least about 75%
 CC identity with any of these or its complements; or biologically functional
 CC sequences having conservative amino acid sequence changes. The nucleic
 CC acid molecules encoding the amino acid transporters are useful for
 CC altering the activity of the amino acid transporters in a plant, or for
 CC producing a plant tissue with an increased amino acid content. The
 CC transformed plants or plant parts are useful in providing new and
 CC improved food and feed for human and animal nutrition needs. The nucleic
 CC acid molecules may also be used to obtain nucleic acid homologues, or to
 CC isolate promoters of cell enhanced, cell specific, tissue enhanced,
 CC tissue specific, developmentally or environmentally regulated expression
 CC profiles. This sequence corresponds to one of the proteins of the
 CC invention.
 XX
 SQ Sequence 462 AA;
 Query Match 58.1%; Score 36; DB 7; Length 462;
 Best Local Similarity 54.5%; Pred. No. 1.2e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RLCRIVVIRVC 11
 | | | | : |||
 Db 365 RACRVNPLRVC 375
 RESULT 86
 ADT58108
 ID ADT58108 standard; protein; 471 AA.
 XX
 AC ADT58108;
 XX
 XX 13-JAN-2005 (first entry)
 XX
 DE Plant polypeptide, SEQ ID 8185.
 XX
 KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
 KW disease resistance; galactomannan production; plant growth regulator;
 KW heat tolerance; herbicide tolerance; lignin production;
 KW extreme osmotic condition tolerance; pathogens resistance;
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.
 XX
 OS Viridiplantae.
 XX
 XX US2004216190-A1.
 XX
 XX 28-OCT-2004.
 XX
 XX 18-DEC-2003; 2003US-00739930.
 XX
 XX 28-APR-2003; 2003US-00424599.
 XX 28-APR-2003; 2003US-00425115.
 XX
 PA (KOVA/) KOVALIC D K.
 XX
 PI Kovalic DK;
 XX
 XX WPI; 2004-757369/74.
 XX
 XX New recombinant DNA constructs useful in the field of biochemistry and
 PT genetics, and in particular for producing transgenic plants with improved
 PT biological characteristics.

XX Claim 2; SEQ ID NO 8185; 14pp; English.
 XX
 CC The invention relates a recombinant DNA construct comprising a
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
 CC Arabidopsis, wheat and rape but the specification does not indicate which
 CC sequences is derived from which organism. Also included is a method of
 CC producing a plant having an improved property, comprising transforming a
 CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle
 CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 5544 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.
 XX
 SQ Sequence 471 AA;
 Query Match 58.1%; Score 36; DB 8; Length 471;
 Best Local Similarity 54.5%; Pred. No. 1.2e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RLCRIVVIRVC 11
 | | | | : |||
 Db 372 RACRVNPLRVC 382
 RESULT 87
 ADX68104
 ID ADX68104 standard; protein; 517 AA.
 XX
 AC ADX68104;
 XX
 XX 21-APR-2005 (first entry)
 XX
 XX Plant full length insert polypeptide seqid 38947.
 DE
 XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.
 XX

PN US2004034888-A1.
 XX 19-FEB-2004.
 XX 28-APR-2003; 2003US-00425114.
 XX 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAOY/) CAO Y.
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX Claim 1; SEQ ID NO 38947; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX SQ Sequence 517 AA;
 Query Match 58.1%; Score 36; DB 8; Length 517;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 CRIVVIRVCR 12
 Db 232 CRVVVKKSCR 241
 RESULT 88
 ADJ48834
 ID ADJ48834 standard; protein; 537 AA.
 XX ADJ48834;
 AC ADJ48834;
 XX 06-MAY-2004 (first entry)
 DT Oil-associated gene related protein #334.
 DE oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
 KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
 XX Unidentified.
 OS Unidentified.
 XX US2004025202-A1.
 PN

PD 05-FEB-2004.
 XX 14-MAR-2003; 2003US-00389566.
 XX 15-MAR-2002; 2002US-0365301P.
 PR 26-JUN-2002; 2002US-0391786P.
 PR 26-JUN-2002; 2002US-0392018P.
 XX (LAUR/) LAURIE C C.
 PA (RAVA/) RAVANELLO M.
 PA (SAVA/) SAVAGE T.
 PA (LEDE/) LEDEAUX J R.
 PA (ROGE/) ROGERS J A.
 XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
 PI WPI; 2004-142683/14.
 XX Novel recombinant DNA construct comprising a promoter functional in
 PT plants operably linked to an oil-associated gene for producing transgenic
 PT plant seed.
 XX Example 3; SEQ ID NO 838; 22pp; English.
 PS The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in plants operably linked to an oil-associated gene.
 CC The construct is useful for transgenic plant seed which has in its genome
 CC the construct, that is functional in the plant to transcribe the oil-
 CC associated gene. The transgenic plant seed grows into a plant having
 CC enhanced seed oil as compared to wild type. The construct is useful for
 CC producing hybrid maize seed. The transgenic plant seed is useful for
 CC producing vegetable oil. The present sequence represents the amino acid
 CC sequence of an oil-associated gene related protein.
 XX SQ Sequence 537 AA;
 Query Match 58.1%; Score 36; DB 8; Length 537;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 LCRIVVIRVCR 12
 Db 277 MCRVSWTRVCR 287
 RESULT 89
 ADT60441
 ID ADT60441 standard; protein; 645 AA.
 XX ADT60441;
 AC ADT60441;
 XX 13-JAN-2005 (first entry)
 DT Plant polypeptide, SEQ ID 10518.
 DE Plant; transgenic; cold tolerance; growth rate; drought tolerance;
 XX disease resistance; galactomannan production; plant growth regulator;
 KW heat tolerance; herbicide tolerance; lignin production;
 KW extreme osmotic condition tolerance; pathogens resistance;
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.
 XX Viridiplantae.
 OS US2004216190-A1.
 XX 28-OCT-2004.
 PD 18-DEC-2003; 2003US-00739930.
 PF 28-APR-2003; 2003US-00424599.
 PR 28-APR-2003; 2003US-00425115.
 XX (KOVA/) KOVALIC D K.
 PA

XX PI Kovalic DK;
 XX DR WPI; 2004-757369/74.
 XX
 XX New recombinant DNA constructs useful in the field of biochemistry and
 PT genetics, and in particular for producing transgenic plants with improved
 PT biological characteristics.
 XX
 XX Claim 2; SEQ ID NO 10518; 14pp; English.
 XX
 XX The invention relates a recombinant DNA construct comprising a
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
 CC Arabidopsis, wheat and rape but the specification does not indicate which
 CC sequences is derived from which organism. Also included is a method of
 CC producing a plant having an improved property, comprising transforming a
 CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle
 CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 5544 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20040216190.
 XX
 XX Sequence 645 AA;
 SQ
 Query Match 58.1%; Score 36; DB 8; Length 645;
 Best Local Similarity 60.0%; Pred. No. 1.6e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LCRIVIRVC 11
 :|||:
 Db 182 ICRGVINAC 191
 RESULT 90
 ADM48165
 ID ADM48165 standard; protein; 709 AA.
 XX
 XX ADM48165;
 AC
 XX 03-JUN-2004 (first entry)
 DT
 XX Polypeptide sequence #215 useful in producing transgenic plants.
 DE
 XX Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
 KW osmotic stress; sugar transport; cell cycle pathway; plant height;
 KW carbohydrate transport; crop productivity; plant growth;
 .KW

KW stress resistance; disease resistance; insect resistance; heat tolerance;
 KW nitrogen assimilation; water stress tolerance;
 KW photosynthetic carbon fixation; virus resistance; gene therapy.
 XX
 OS Oryza sativa.
 XX
 PN US2003233670-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 04-DEC-2002; 2002US-00310154.
 XX
 PR 04-DEC-2001; 2001US-0337358P.
 XX
 PA (EDGE/) EDGERTON M D.
 PA (CHOM/) CHOMET P S.
 PA (LACC/) LACCETTI L B.
 XX
 PI Edgerton MD, Chomet PS, Laccetti LB;
 XX
 XX WPI; 2004-061374/06.
 DR N-PSDB; ADM47797.
 XX
 XX New polynucleotide, useful for manipulating plant protein quality,
 PT improving plant growth, yield and crop productivity or grain composition
 PT or producing plants with improved properties.
 XX
 XX Claim 8; SEQ ID NO 583; 144pp; English.
 XX
 CC The present invention relates to polynucleotide sequences, and the
 CC proteins they encode. The sequences are isolated from a variety of
 CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
 CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
 CC polynucleotide and polypeptide sequences of the invention are useful in
 CC the production of transgenic plants that have improved properties. Also
 CC disclosed are methods of producing fertile transgenic plants, preferably
 CC maize, with desired phenotypes. The polynucleotide and polypeptide
 CC sequences are useful for improving plants by providing protection against
 CC osmotic stress, improving altering sugar transport and/or metabolism,
 CC modifying the cell cycle pathway, reducing plant height, modifying
 CC carbohydrate transport, improving crop productivity, improving plant
 CC growth and stress resistance, improving disease resistance, improving
 CC insect resistance, improving cold or heat tolerance, improving nitrogen
 CC assimilation, improving stalk strength, improving water stress tolerance,
 CC improving photosynthetic carbon fixation, improving biotic and abiotic
 CC stress resistance, improving resistance to oxidative stress, providing
 CC increased vigour, reducing senescence, and conferring virus resistance.
 CC The present sequence represents a polypeptide sequence of the invention.
 CC Note: The sequence data for this patent is not provided in the printed
 CC specification but is obtained in electronic format from the USPTO website
 CC at seqdata.uspto.gov.
 XX
 XX Sequence 709 AA;
 SQ
 Query Match 58.1%; Score 36; DB 8; Length 709;
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CRIVIRVCR 12
 ||-||-||
 Db 387 CRIVIRKSCR 396
 RESULT 91
 ABB58525
 ID ABB58525 standard; protein; 762 AA.
 XX
 XX ABB58525;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 2367.
 DE
 XX

KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX Drosophila melanogaster.

OS WO200171042-A2.

PN 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

PA Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL02628.

XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.

PS Disclosure; SEQ ID NO 2367; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 762 AA;

Query Match 58.1%; Score 36; DB 4; Length 762;

Best Local Similarity 45.5%; Pred. No. 1.9e+03;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVC 11

Db 28 RVCRVFIRQC 38

RESULT 92

ADW38367 ID ADW38367 standard; protein; 861 AA.

XX AC ADW38367;

XX 24-MAR-2005 (first entry)

DE Ancestral FIV subtype B envelope (env) SEQ ID NO 22.

XX virucide; vaccine; diagnosis; FIV infection; envelope; env.

XX Feline immunodeficiency virus.

OS Synthetic.

PN WO2005001029-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015816.

XX 19-MAY-2003; 2003US-00441926.

PA (AUCK-) AUCKLAND UNISERVICES LTD.

PA (UNIW) UNIV WASHINGTON.

XX Mullins JI, Rodrigo A, Ross HA;

XX WPI; 2005-075527/08.

DR N-PSDB; ADW38366.

XX New ancestral feline immunodeficiency virus (FIV) nucleic acid sequence or its fragment that is a determined founder sequence of a highly diverse viral strain, subtype or group, useful in preparing a vaccine against FIV.

PS Claim 5; SEQ ID NO 22; 225pp; English.

XX The invention describes a new isolated ancestral feline immunodeficiency virus (FIV) nucleic acid sequence or its fragment is a determined founder sequence of a highly diverse viral strain, subtype or group. Also described are: an isolated ancestor protein or its fragment from FIV; an isolated expression construct comprising the operably linked elements consisting of a transcriptional promoter, a nucleic acid encoding an FIV ancestor protein and a transcriptional terminator; a cultured prokaryotic or eukaryotic cell transformed or transfected with the expression construct; a composition for inducing an immune response in a mammal comprising a highly diverse FIV ancestor protein or its antigenic fragment; a method of preparing an FIV viral amino acid sequence; a method for inducing an immune response to FIV in a host; a method for making an FIV vaccine; a kit comprising a composition comprising an FIV ancestor protein or an antigenic fragment of an FIV ancestor protein and instructions for administering the composition to a subject; and a method for detecting infection with FIV. The ancestral feline immunodeficiency virus (FIV) nucleic acid sequence is useful in preparing a vaccine against FIV. This is the amino acid sequence of an ancestral FIV subtype B envelope (env) protein.

XX SQ Sequence 861 AA;

Query Match 58.1%; Score 36; DB 9; Length 861;

Best Local Similarity 54.5%; Pred. No. 2.1e+03;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVC 11

Db 147 RNCRLITIAIC 157

RESULT 93

ADW38369 ID ADW38369 standard; protein; 861 AA.

XX AC ADW38369;

XX 24-MAR-2005 (first entry)

DE Ancestral FIV subtype B envelope (env) SEQ ID NO 24.

XX virucide; vaccine; diagnosis; FIV infection; envelope; env.

XX Feline immunodeficiency virus.

OS Synthetic.

PN WO2005001029-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015816.

XX 19-MAY-2003; 2003US-00441926.

XX (AUCK-) AUCKLAND UNISERVICES LTD.

XX (UNIW) UNIV WASHINGTON.

XX Mullins JI, Rodrigo A, Ross HA;

DR WPI; 2005-075527/08.
 DR N-PSDB; ADW38368.
 XX
 PT New ancestral feline immunodeficiency virus (FIV) nucleic acid sequence
 PT or its fragment that is a determined founder sequence of a highly diverse
 PT viral strain, subtype or group, useful in preparing a vaccine against
 PT FIV.
 XX
 XX Claim 5; SEQ ID NO 24; 225pp; English.
 XX
 CC The invention describes a new isolated ancestral feline immunodeficiency
 CC virus (FIV) nucleic acid sequence or its fragment is a determined founder
 CC sequence of a highly diverse viral strain, subtype or group. Also
 CC described are: an isolated ancestor protein or its fragment from FIV; an
 CC isolated expression construct comprising the operably linked elements
 CC consisting of a transcriptional promoter, a nucleic acid encoding an FIV
 CC ancestor protein and a transcriptional terminator; a cultured prokaryotic
 CC or eukaryotic cell transformed or transfected with the expression
 CC construct; a composition for inducing an immune response in a mammal
 CC comprising a highly diverse FIV ancestor protein or its antigenic
 CC fragment; a method of preparing an FIV viral amino acid sequence; a
 CC method for inducing an immune response to FIV in a host; a method for
 CC making an FIV vaccine; a kit comprising a composition comprising an FIV
 CC ancestor protein or an antigenic fragment of an FIV ancestor protein and
 CC instructions for administering the composition to a subject; and a method
 CC for detecting infection with FIV. The ancestral feline immunodeficiency
 CC virus (FIV) nucleic acid sequence is useful in preparing a vaccine
 CC against FIV. This is the amino acid sequence of an ancestral FIV subtype
 CC B envelope (env) protein.
 XX
 SQ Sequence 861 AA;
 Query Match 58.1%; Score 36; DB 9; Length 861;
 Best Local Similarity 54.5%; Pred. No. 2.1e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RLCRIVVIRVC 11
 Db | | | | | : | : |
 147 RNCRIILTIAIC 157
 RESULT 94
 ADW38365
 ID ADW38365 standard; protein; 861 AA.
 XX AC ADW38365;
 XX
 XX 24-MAR-2005 (first entry)
 DT
 XX Ancestral FIV subtype B envelope (env) SEQ ID NO 20.
 DE
 XX virucide; vaccine; diagnosis; FIV infection; envelope; env.
 KW
 XX Feline immunodeficiency virus.
 OS Synthetic.
 XX
 XX WO2005001029-A2.
 PN
 XX 06-JAN-2005.
 PD
 XX 19-MAY-2004; 2004WO-US015816.
 PF
 XX 19-MAY-2003; 2003US-00441926.
 XX
 XX (AUCK-) AUCKLAND UNISERVICES LTD.
 PA (UNIW) UNIV WASHINGTON.
 PA
 XX Mullins JI, Rodrigo A, Ross HA;
 PI
 XX WPI; 2005-075527/08.
 XX N-PSDB; ADW38364.
 DR
 XX New ancestral feline immunodeficiency virus (FIV) nucleic acid sequence

PT or its fragment that is a determined founder sequence of a highly diverse
 PT viral strain, subtype or group, useful in preparing a vaccine against
 PT FIV.
 XX
 XX Claim 5; SEQ ID NO 20; 225pp; English.
 XX
 CC The invention describes a new isolated ancestral feline immunodeficiency
 CC virus (FIV) nucleic acid sequence or its fragment is a determined founder
 CC sequence of a highly diverse viral strain, subtype or group. Also
 CC described are: an isolated ancestor protein or its fragment from FIV; an
 CC isolated expression construct comprising the operably linked elements
 CC consisting of a transcriptional promoter, a nucleic acid encoding an FIV
 CC ancestor protein and a transcriptional terminator; a cultured prokaryotic
 CC or eukaryotic cell transformed or transfected with the expression
 CC construct; a composition for inducing an immune response in a mammal
 CC comprising a highly diverse FIV ancestor protein or its antigenic
 CC fragment; a method of preparing an FIV viral amino acid sequence; a
 CC method for inducing an immune response to FIV in a host; a method for
 CC making an FIV vaccine; a kit comprising a composition comprising an FIV
 CC ancestor protein or an antigenic fragment of an FIV ancestor protein and
 CC instructions for administering the composition to a subject; and a method
 CC for detecting infection with FIV. The ancestral feline immunodeficiency
 CC virus (FIV) nucleic acid sequence is useful in preparing a vaccine
 CC against FIV. This is the amino acid sequence of an ancestral FIV subtype
 CC B envelope (env) protein.
 XX
 SQ Sequence 861 AA;
 Query Match 58.1%; Score 36; DB 9; Length 861;
 Best Local Similarity 54.5%; Pred. No. 2.1e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RLCRIVVIRVC 11
 Db | | | | | : | : |
 147 RNCRIILTIAIC 157
 RESULT 95
 AAM41078
 ID AAM41078 standard; protein; 913 AA.
 XX AC AAM41078;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 XX Human polypeptide SEQ ID NO 6009.
 DE
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 KW
 XX Homo sapiens.
 OS
 XX WO200153312-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 26-DEC-2000; 2000WO-US034263.
 PF
 XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00655450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.

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XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou F, Goodrich R, Drmanac RT;
XX DR WPI; 2001-442253/47.
XX N-PSDB; AAI60234.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX PS Example 2; SEQ ID NO 6009; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM9642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX SQ Sequence 913 AA;

Query Match 58.1%; Score 36; DB 4; Length 913;
Best Local Similarity 55.6%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
Db 768 CRLVLRWC 776
||:|:|

RESULT 96
ADSI2128
ID ADS12128 standard; protein; 913 AA.
XX AC ADS12128;
XX DT 16-DEC-2004 (first entry)
XX DE Human therapeutic contig protein - SEQ ID 2365.
XX KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX Misc-difference 1..913
XX /label= Unknown, OTHER
XX /note= "OTHER = In-frame STOP codon"
XX WO2004080148-A2.
XX PD 23-SEP-2004.
XX PF 30-SEP-2003; 2003WO-US030720.
XX PR 02-OCT-2002; 2002US-0416186P.
XX PA (NUVE-) NUVELO INC.
XX PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

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XX WPI; 2004-668857/65.
XX N-PSDB; ADS11530.
XX PT New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.
XX PS Example 2; SEQ ID NO 2365; 718pp; English.
XX CC The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic contig
XX protein of the invention.
XX SQ Sequence 913 AA;

Query Match 58.1%; Score 36; DB 8; Length 913;
Best Local Similarity 55.6%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
Db 768 CRLVLRWC 776
||:|:|

RESULT 97
ABMS5214
ID ABM85214 standard; protein; 123 AA.
XX AC ABM85214;
XX DT 18-NOV-2004 (first entry)
XX DE Mouse protein sequence MCP18249.
XX KW Cytostatic; carcinoma; lymphoma; cancer; murine.
XX OS Mus musculus.
XX FN WO2003073826-A2.
XX PD 12-SEP-2003.
XX PF 28-FEB-2003; 2003WO-US006235.
XX PR 01-MAR-2002; 2002US-00087192.
XX PA (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW;
XX WPI; 2003-328604/31.
XX PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX comprises a nucleotide sequence.
XX PS Claim 5; SEQ ID NO 57; 0pp; English.
XX CC The present invention relates to novel DNA and protein sequences which
XX are associated with carcinomas. The sequences are useful for: (i) for
XX screening drug candidates; (ii) for screening of bioactive agent capable
XX of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
XX a bioactive agent capable of modulating the activity of CAP; (iv) for
XX evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
XX carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
XX carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
XX (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for

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CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CAP. Note:
CC This patent is an equivalent to basic patent US2002182586A1, for which no
CC sequence data was published
XX
SQ Sequence 123 AA;

Query Match 56.5%; Score 35; DB 7; Length 123;
Best Local Similarity 40.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVVIRVC 11
DB 113 VCRVVCVKAC 122
:|:|:|:|:|:|

RESULT 98
ABM89108
ID ABM89108 standard; protein; 190 AA.
XX
AC ABM89108;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7354.
XX
KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX
OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 7354; 89pp; English.

XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX

SQ Sequence 190 AA;
Query Match 56.5%; Score 35; DB 7; Length 190;

Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVVIRVC 11
DB 103 LCRVQLRLIC 112
|||:|:|

RESULT 99
ABG16152
ID ABG16152 standard; protein; 208 AA.
XX
AC ABG16152;

XX DT 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #16143.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.
XX
PN WO200175067-A2.

XX PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.

XX PF 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.
DR N-PSDB; AAS80339.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 46511; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 208 AA;

Query Match 56.5%; Score 35; DB 4; Length 208;
Best Local Similarity 50.0%; Pred. No. 8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy	1	RLCRIVIRVCR	12
		: : :	
		: : :	
Db	15	RVCSALPKVCR	26
RESULT 100			
AAW37840			
ID	AAW37840	standard; protein; 228 AA.	
XX	AAW37840;		
XX	28-JUL-1998	(first entry)	
XX	Truncated human 312C2	protein from clone A8	amino acid sequence.
XX	Human 312C2	T cell protein; thymus cell; spleen cell; T cell;	
KW	antigen-specific T cell	proliferation; cytokine production by T-cell;	
KW	apoptosis; cancer; haematopoietic cells;	lymphoid cell;	
KW	autoimmune disorders.		
XX	Homo sapiens.		
OS	WO9806842-A1.		
XX	19-FEB-1998.		
XX	14-AUG-1997;	97WO-US013931.	
XX	16-AUG-1996;	96US-00689943.	
PR	07-OCT-1996;	96US-0027901P.	
XX	(SCHE) SCHERING CORP.		
PA	Gorman DM, Randall TD, Zlotnik A;		
XX	WPI; 1998-159534/14.		
XX	N-PSDB; AAV19154.		
DR	Isolated 312C2 T cell gene -	used to develop products for treating, e.g.	
PT	cancers, auto-immune disorders,	transplantation rejection and other T	
PT	cell disorders.		
PT	Disclosure; Page 61-62; 71pp; English.		
PS	This is the amino acid sequence of the truncated human 312C2 T cell		
XX	protein from clone A8. The 312C2 proteins are expressed in thymus cells		
CC	and are induced on T cells and spleen cells following activation.		
CC	Engagement of 312C2 stimulates proliferation of T cell clones, antigen-		
CC	specific proliferation and cytokine production by T-cells, and		
CC	potentiates T cell expansion or apoptosis. The products can be used in		
CC	the treatment of conditions associated with abnormal physiology or		
CC	development, including abnormal proliferation, e.g. cancerous conditions		
CC	or degenerative conditions. They can be used in the regulation or		
CC	development of haematopoietic cells, e.g. lymphoid cells which affect		
CC	immunological responses, e.g. autoimmune disorders		
XX	Sequence 228 AA;		
SQ	Query Match	56.5%;	Score 35; DB 2; Length 228;
	Best Local Similarity	50.0%;	Pred. No. 8.7e+02;
	Matches	6; Conservative	1; Mismatches 5; Indels 0; Gaps 0;
Qy	1	RLCRIVIRVCR	12
		: : :	
		: : :	
Db	42	RCRCVHTTRCCR	53

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 11:06:26 ; Search time 38 Seconds
(without alignments)
30.384 Million cell updates/sec

Title: US-10-657-851-37
Perfect score: 62
Sequence: 1 RLCRIVIVRVC 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	155	2 S27018	bactenecin precurs
2	52	83.9	155	2 S68229	antimicrobial pept
3	42	67.7	662	2 T00497	polyadenylate-bind
4	38	61.3	2102	2 T15626	hypothetical prote
5	36	58.1	165	2 S72595	hypothetical prote
6	36	58.1	219	2 G87371	hypothetical prote
7	36	58.1	276	2 T44181	hypothetical prote
8	36	58.1	276	2 T43994	virion protein lim
9	36	58.1	344	2 T23374	hypothetical prote
10	36	58.1	391	2 S48967	ethanolaminephosph
11	35.5	57.3	2761	2 T21064	hypothetical prote
12	35	56.5	218	2 C72747	probable endonucle
13	35	56.5	414	2 A22242	hypothetical prote
14	35	56.5	505	2 A81806	probable two compo
15	35	56.5	1007	2 G96606	disease resistance
16	34	54.8	143	2 T34647	probable integral
17	34	54.8	152	2 P80427	napin AHI precurs
18	34	54.8	153	2 J01491	hypothetical 16.2K
19	34	54.8	174	2 P80435	napin BAJ precurs
20	34	54.8	188	2 S25979	ribosomal protein
21	34	54.8	209	2 G98075	phosphoribosylanth
22	34	54.8	237	2 S55614	hypothetical prote
23	34	54.8	254	2 A13176	transcription regu
24	34	54.8	268	2 H84684	En/Spm-like transp
25	34	54.8	301	2 T44011	G protein-coupled
26	34	54.8	310	2 T33205	hypothetical prote
27	34	54.8	505	2 H81064	sensor histidine k
28	34	54.8	810	1 P2WMBB	2a protein - broad
29	34	54.8	1717	2 T50247	probable helicase

30	33.5	54.0	550	2	G86225	hypothetical prote
31	33	53.2	191	2	B82903	hypothetical prote
32	33	53.2	200	2	S35292	hypothetical prote
33	33	53.2	224	2	F69937	conserved hypotet
34	33	53.2	254	1	H69454	enoyl-CoA hydratase
35	33	53.2	273	2	AH2432	hypothetical prote
36	33	53.2	279	2	B81599	hypothetical prote
37	33	53.2	279	2	A86555	hypothetical prote
38	33	53.2	279	2	C72070	hypothetical prote
39	33	53.2	291	2	T47475	hypothetical prote
40	33	53.2	346	2	AB3057	conserved hypotet
41	33	53.2	346	2	D98229	hypothetical prote
42	33	53.2	349	2	T29843	hypothetical prote
43	33	53.2	468	2	A56856	retinoid-related o
44	33	53.2	480	2	B56182	fibroblast growth
45	33	53.2	480	2	A56182	fibroblast growth
46	33	53.2	515	2	T08539	hypothetical prote
47	33	53.2	575	2	T12094	beta-fructofuranos
48	33	53.2	629	2	T05425	polyadenylate-bind
49	33	53.2	638	2	S37085	polyadenylate-bind
50	33	53.2	646	2	B70396	histidine kinase s
51	33	53.2	658	2	H95852	hypothetical fusio
52	33	53.2	813	1	A49123	fibroblast growth
53	33	53.2	951	2	T04492	protein kinase hom
54	33	53.2	1378	2	T47605	RING finger-like p
55	32.5	52.4	365	2	S43417	RNA/DNA-binding pr
56	32.5	52.4	405	1	QB8E35	BBRF3 protein - hu
57	32.5	52.4	954	2	T02657	hypothetical prote
58	32.5	52.4	1732	2	G84664	hypothetical prote
59	32	51.6	112	2	T25554	hypothetical prote
60	32	51.6	122	2	T07522	ribosomal protein
61	32	51.6	145	2	F75337	transposase - Dein
62	32	51.6	157	2	S31078	seed allergen RA5
63	32	51.6	161	2	AC0883	conserved hypotet
64	32	51.6	162	2	AB2644	flagellar protein
65	32	51.6	220	2	T12510	hypothetical prote
66	32	51.6	226	2	AC2825	transcription regu
67	32	51.6	231	2	B97603	hypothetical prote
68	32	51.6	274	2	D75362	Far-related protei
69	32	51.6	277	2	T27597	hypothetical prote
70	32	51.6	338	2	T27662	hypothetical prote
71	32	51.6	350	2	C72711	hypothetical prote
72	32	51.6	377	2	T05427	hypothetical prote
73	32	51.6	390	2	T21367	hypothetical prote
74	32	51.6	394	2	S75996	hypothetical prote
75	32	51.6	396	2	AF0791	probable transmem
76	32	51.6	443	2	I38603	heme A farnesyltra
77	32	51.6	498	2	B82622	anthranilate synth
78	32	51.6	536	2	T37840	probable vacuolar
79	32	51.6	570	2	S70773	cytochrome B245 be
80	32	51.6	655	2	T00768	polyadenylate-bind
81	32	51.6	671	2	C96534	probable Poly-A Bi
82	32	51.6	685	2	A59348	formate dehydrogen
83	32	51.6	1175	2	T34182	hypothetical prote
84	32	51.6	1513	2	T23681	hypothetical prote
85	32	51.6	3051	2	S42373	hypothetical prote
86	32	51.6	3511	2	A59295	unconventional myo
87	32	51.6	3530	2	A59266	unconventional myo
88	32	51.6	3856	2	T51174	ataxia-telangiecta
89	31.5	50.8	196	2	H71263	hypothetical prote
90	31.5	50.8	1737	2	T17101	probable voltage-a
91	31	50.0	62	2	D81789	hypothetical prote
92	31	50.0	108	2	F82564	hypothetical prote
93	31	50.0	111	1	B0RT1	prostatic steroid-
94	31	50.0	122	1	R5LV14	ribosomal protein
95	31	50.0	122	1	R5SP14	ribosomal protein
96	31	50.0	134	2	H83005	hypothetical prote
97	31	50.0	136	2	C72524	hypothetical prote
98	31	50.0	142	2	S40195	ribosomal protein
99	31	50.0	250	2	T03115	probable fusion pr
100	31	50.0	290	2	H71950	hypothetical prote

ALIGNMENTS

RESULT 1

S27018
bactenecin precursor - bovine
N;Alternate names: antibiotic dodecapeptide
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: S27018; A33799
R;Scorici, P.; del Sal, G.; Schneider, C.; Zanetti, M.
FEBS Lett. 314, 187-190, 1992
A;Title: cDNA sequence analysis of an antibiotic dodecapeptide from neutrophils.
A;Reference number: S27018; MUID:93093170; PMID:1459251
A;Accession: S27018
A;Molecule type: mRNA
A;Residues: 1-155 <STO>
A;Cross-references: UNIPROT:P22226; UNIPARC:UPI0000049485; GB:L08834; NID:G162599; PIDN:
A;Experimental source: bone marrow
R;Romeo, D.; Skerlavaj, B.; Bolognesi, M.; Gennaro, R.
J. Biol. Chem. 263, 9573-9575, 1988
A;Title: Structure and bactericidal activity of an antibiotic dodecapeptide purified from
A;Reference number: A33799; MUID:98257074; PMID:3290210
A;Accession: A33799
A;Molecule type: protein
A;Residues: 144-155 <ROM>
A;Cross-references: UNIPARC:UPI000003532B
A;Experimental source: neutrophils
C;Superfamily: cathelin; cystatin homology
C;Keywords: antibacterial
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-143/Domain: propeptide #status predicted <PRO>
F;144-155/Product: bactenecin #status experimental <MAT>
F;146-154/Disulfide bonds: #status experimental

Query Match 100.0%; Score 62; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRCRIVVRVCR 12

Db 144 LRCRIVVRVCR 155

RESULT 2

S68229
antimicrobial peptide precursor - sheep
N;Alternate names: procyclic dodecapeptide homolog
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68229
R;Bagella, L.; Scocchi, M.; Zanetti, M.
FEBS Lett. 376, 225-228, 1995
A;Title: cDNA sequences of three sheep myeloid cathelicidins.
A;Reference number: S68228; MUID:96105386; PMID:7498547
A;Accession: S68229
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <BAG>
A;Cross-references: UNIPROT:P54230; UNIPARC:UPI0000126859; EMBL:L46853; NID:G1161246; PIDN:
C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;29-143/Domain: propeptide #status predicted <PRO>
F;144-155/Product: antimicrobial peptide #status predicted <MAT>

Query Match 83.9%; Score 52; DB 2; Length 155;
Best Local Similarity 66.7%; Pred. No. 0.042;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRCRIVVRVCR 12

| : | : | : | : |

Db 144 RICRIIFLRVCR 155

RESULT 3

T00497
polyadenylate-binding protein At2g23350 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00497; F84623
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.L.;
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84623
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-662 <STO>
A;Cross-references: UNIPROT:O221173; UNIPARC:UPI00000A0BE1; EMBL:AC002391; NID:G2642427; I
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.L.
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: F84623

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-662 <STO>

A;Cross-references: UNIPARC:UPI00000A0BE1; GB:AE002093; NID:G2642429; PIDN:AA887097.1; G

C;Genetics:

A;Gene: T20D16.2; At2g23350

A;Map position: 2

A;Introns: 100/1; 139/3; 358/3; 384/3; 414/3; 459/3; 515/3; 576/3

C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

C;Keywords: nucleus; RNA binding

F;226-292/Domain: ribonucleoprotein repeat homology <RRM3>

Query Match 67.7%; Score 42; DB 2; Length 662;

Best Local Similarity 54.5%; Pred. No. 7.9;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVVRVCR 12

| : | : | : | : |

Db 69 VCQVSVRVCR 79

RESULT 4

T15626
hypothetical protein C25H3.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15626
R;Johnson, D.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid C25H3.
A;Reference number: Z18379
A;Accession: T15626
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2102 <JOH>
A;Cross-references: UNIPARC:UPI00001640A2; EMBL:U29535; NID:G868251; PIDN:AF
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CTSP:C25H3.8
A;Introns: 400/2; 464/1; 613/3; 669/3; 682/1; 927/1; 1266/3; 1403/3; 1595/1; 1625/1; 1764

Query Match 61.3%; Score 38; DB 2; Length 2102;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVVRVCR 12

| : | : | : | : |

Db 1966 LCRVRIPCLR 1976

RESULT 5

S72595

hypothetical protein B1937_F2_40 - Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

A:Accession: S72595; T10043

R:Smith, D.R.; Robison, K.

submitted to the EMBL Data Library, November 1993

A:Reference number: S72580

A:Accession: S72595

A:Molecule type: DNA

A:Residues: 1-165 <SMI>

A:Cross-references: UNIPROT:Q49758; UNIPARC:UPI00000BEE84; EMBL:U00016; NID:g466961; PID

R:Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z16918

A:Accession: T10043

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-165 <PAR>

A:Cross-references: UNIPARC:UPI00000BEE84; EMBL:Z99125; NID:g2398683; PIDN:CAB16145.1; E

C:Genetics:

A:Start codon: GTG

A:Note: MLC1536.02c

C:Superfamily: Mycobacterium leprae hypothetical protein B1937_F2_40

Query Match

Best Local Similarity 58.1%; Score 36; DB 2; Length 165;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 12

||||: |||

Db 62 RLCQLGSDRVC 73

RESULT 6

G87371

hypothetical protein CC0987 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: G87371

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87371

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-219 <STO>

A:Cross-references: UNIPROT:Q9A9J3; UNIPARC:UPI00000C722F; GB:AE005673; NID:gl3422271; E

C:Genetics:

A:Gene: CC0987

Query Match

Best Local Similarity 58.1%; Score 36; DB 2; Length 219;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11

||||: |||

Db 174 RCRVIOARLC 184

RESULT 7

T44181

hypothetical protein U34 [imported] - human herpesvirus 6 (strain Z29)

C:Species: human herpesvirus 6

A:Variety: strain Z29

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000

C:Accession: T44181

R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.

J. Virol. 73, 8040-8052, 1999

A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human 1

A:Reference number: Z22734; MUID:99412318; PMID:10482553

A:Accession: T44181

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-276 <DOM>

A:Cross-references: UNIPARC:UPI00000F46EE; EMBL:AF157706; PIDN:AAD49648.1

A:Experimental source: strain Z29; variant B

C:Genetics:

A:Note: U34

Query Match

Best Local Similarity 58.1%; Score 36; DB 2; Length 276;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11

||||: |||

Db 242 RHCRAIVSIC 252

RESULT 8

T43994

virion protein [imported] - human herpesvirus 6 (strain HST)

C:Species: human herpesvirus 6

A:Variety: strain HST

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43994

R:Iseigawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa

J. Virol. 73, 8053-8063, 1999

A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and E

A:Reference number: Z22732; MUID:99412319; PMID:10482554

A:Accession: T43994

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-276 <ISE>

A:Cross-references: UNIPROT:Q9WT30; UNIPARC:UPI000000ECC92; EMBL:AB021506; NID:g4995977; I

A:Experimental source: strain HST; pop. variant B

C:Genetics:

A:Note: U34

Query Match

Best Local Similarity 58.1%; Score 36; DB 2; Length 276;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11

||||: |||

Db 242 RHCRAIVSIC 252

RESULT 9

T23374

hypothetical protein K06G5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T23374

R:Mortimore, B.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19733

A:Accession: T23374

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-344 <WIL>

A:Cross-references: UNIPROT:Q9XU00; UNIPARC:UPI000007B9CC; EMBL:Z81565; PIDN:CAB04580.1;

A:Experimental source: clone K06G5

C:Genetics:

A:Gene: CESP:K06G5.3

A:Map position: X

A:Introns: 22/3; 68/3; 91/3; 108/3; 131/3; 154/3; 179/3; 203/3; 236/3; 260/3; 280/3; 302/

Query Match 58.1%; Score 36; DB 2; Length 344;

Best Local Similarity 50.0%; Pred. No. 54;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVIRVC 11
|||:|:|
Db 55 LCBIIVSKIC 64

RESULT 10
ethanolaminephosphotransferase (EC 2.7.8.1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR123w; sn-1,2-diacylglycerol ethanolamine phosphotransferase
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
C;Accession: S48967; S27296; A23714; S16700
R;Fulton, L.
submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid 9315.
A;Reference number: S48967
A;Accession: S48967
A;Molecule type: DNA
A;Residues: 1-391 <FUL>
A;Cross-references: UNIPROT:P22140; UNIPARC:UPI000012A0BD; EMBL:U10398; NID:G551328; PMID:
R;Hjelmstad, R.H.; Bell, R.M.
submitted to the EMBL Data Library, April 1991
A;Reference number: S27296
A;Accession: S27296
A;Molecule type: DNA
A;Residues: 1-391 <HUE2>
A;Cross-references: UNIPARC:UPI000012A0BD; EMBL:M59311
R;Hjelmstad, R.H.; Bell, R.M.
J. Biol. Chem. 266, 5094-5103, 1991
A;Title: sn-1,2-diacylglycerol choline- and ethanolaminephosphotransferases in Saccharom
A;Reference number: A23714; MUID:91161601; PMID:1848238
A;Accession: A23714
A;Molecule type: DNA
A;Residues: 1-95, 'V', 97, 'S', 99-277, 'ETSDVATKL', 287-391 <HUE>
A;Cross-references: UNIPARC:UPI0000179595; GB:M59311
A;Note: the authors translated the codon GTA for residue 26 as Tyr
A;Note: the sequence from Fig. 7 is inconsistent with that from Fig. 2 in having 278-Leu
C;Genetics:
A;Gene: SGD:EPT1
A;Cross-references: SGD:S0001165; MIPS:YHR123W
A;Map position: 8R
A;Introns: 17/2
C;Superfamily: choline/ethanolaminephosphotransferase
C;Keywords: transferase; transmembrane protein
F;49-69/Domain: transmembrane #status predicted <TM1>
F;175-195/Domain: transmembrane #status predicted <TM2>
F;216-236/Domain: transmembrane #status predicted <TM3>
F;263-283/Domain: transmembrane #status predicted <TM4>
F;289-309/Domain: transmembrane #status predicted <TM5>
F;319-339/Domain: transmembrane #status predicted <TM6>
F;347-367/Domain: transmembrane #status predicted <TM7>

Query Match 58.1%; Score 36; DB 2; Length 391;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVIRVC 11
|||:|:|:|
Db 327 LCQIVLYKIC 336

RESULT 11
T21064
hypothetical protein F53B7.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21064; T22550
R;McMurray, A.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19366

A;Accession: T21064
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2761 <WIL>
A;Cross-references: UNIPROT:Q19522; UNIPARC:UPI0000078341; EMBL:Z72507; PIDN:CAA96634.1;
A;Experimental source: clone F17C11
R;McMurray, A.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19579
A;Accession: T22550
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2761 <WIL2>
A;Cross-references: UNIPARC:UPI0000078341; EMBL:Z72510; PIDN:CAA96654.1; GSPDB:GN00023; C
A;Experimental source: clone F53B7
C;Genetics:
A;Gene: CESP:F53B7.5
A;Map position: 5
A;Introns: 498/1; 543/3; 656/3; 904/1; 1018/1; 1148/1; 1245/1; 1433/3; 1616/1; 1661/3; 16
Query Match 57.3%; Score 35.5; DB 2; Length 2761;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 CRIVIRVC 12
|||||:|
Db 2472 CRIVIRVC-CR 2480

RESULT 12
C72747
probable endonuclease V APE0506 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C72747
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: C72747
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <KAW>
A;Cross-references: UNIPROT:Q9YES5; UNIPARC:UPI000005DB8C; DBJ:AP0000059; NID:G5103911; I
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0506

Query Match 56.5%; Score 35; DB 2; Length 218;
Best Local Similarity 55.6%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVIRVC 11
|||:|:|
Db 32 CRVIRVC 40

RESULT 13
AE2242
hypothetical protein alr3492 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2242
R;Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2242
A;Status: preliminary
A;Molecule type: DNA

Query Match	56.5%	Score 35;	DB 2;	Length 1007;
Best Local Similarity	54.5%;	Pred. No. 1.9e+02;		
Matches 6;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;

RESULT 18
JQ1491
hypothetical 16.2K protein (5' region of estrogen receptor gene) - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: JQ1491
R:Piva, R.; Gambari, R.; Zorzato, F.; Kumar, L.; del Senno, L.
Biochem. Biophys. Res. Commun. 183, 996-1002, 1992
A:Title: Analysis of upstream sequences of the human estrogen receptor gene
A:Reference number: JQ1491; MUID:92231908; PMID:1567414
A:Accession: JQ1491

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-153 <PIV>
A;Cross-references: UNIPROT:Q00849; UNIPARC:UPI000006F875; EMBL:X63118; NID:G35159; PIDN:
C;Superfamily: human hypothetical 16.2K protein (5' region of estrogen receptor gene)

Query Match 54.8%; Score 34; DB 2; Length 153;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CRIVIRVRC 12
| . - : ||||
Db 61 CAVAQLRVC 70

RESULT 19
PS0425
napin RA3 precursor - radish (fragment)
C;Species: Raphanus sativus (radish)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
C;Accession: PS0425
R;Raynal, M.; Depigny, D.; Greillet, F.; Delseny, M.
Gene 99, 77-86, 1991
A;Title: Characterization and evolution of napin-encoding genes in radish and related crucifers
A;Reference number: PS0425; MUID:91216448; PMID:2022325
A;Accession: PS0425
A;Molecule type: mRNA
A;Residues: 1-174 <RAY>
A;Cross-references: UNIPROT:Q41169; UNIPARC:UPI00000A4077; GB:M63843; GB:M36630; NID:G16
A;Experimental source: seed
C;Superfamily: Alpha amylase inhibitor
C;Keywords: storage protein
F;1-28/Domain: signal sequence and propeptide (fragment) #status predicted <PRO>
F;23-63/Product: napin small chain #status predicted <NSC>
F;83-168/Product: napin large chain #status predicted <NLC>

Query Match 54.8%; Score 34; DB 2; Length 174;
Best Local Similarity 45.5%; Pred. No. 72;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVRVRC 11
| . |||| : - |
Db 153 RVCRIPQVSIC 163

RESULT 20
S25979
ribosomal protein L5 - liverwort (Marchantia polymorpha) mitochondrion
C;Species: Marchantia polymorpha
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004
C;Accession: S25979; S41145
R;Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Takemura, M.; Nozato, N.; Akashi, K.; Kar
J. Mol. Biol. 223, 1-7, 1992
A;Title: Gene organization deduced from the complete sequence of liverwort Marchantia po
A;Reference number: S25941; MUID:92114051; PMID:1731062
A;Accession: S25979
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-188 <ODA>
A;Cross-references: UNIPROT:P26860; UNIPARC:UPI00001342B9; EMBL:M68929; NID:G786182; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Takemura, M.; Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Nozato, N.; Akashi, K.; Oh
Nucleic Acids Res. 20, 3199-3205, 1992
A;Title: Gene clusters for ribosomal proteins in the mitochondrial genome of a liverwort
A;Reference number: S41132; MUID:92319654; PMID:1620617
A;Accession: S41145
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-188 <TAK>
A;Cross-references: UNIPARC:UPI00001342B9; EMBL:M68929; NID:G786182; PIDN:AAC09419.1; PT
C;Genetics:
A;Gene: rpl5
A;Genome: mitochondrion

C;Superfamily: ribosomal protein L5/L11
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 54.8%; Score 34; DB 2; Length 188;
Best Local Similarity 62.5%; Pred. No. 76;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIVVI 8
| ||| : ||
Db 35 RLCKIIIV 42

RESULT 21
G98075
phosphoribosylanthranilate isomerase (EC 5.3.1.24) [imported] - Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: G98075
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Be
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: G98075
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-209 <KUR>
A;Cross-references: UNIPROT:Q8DNM7; UNIPARC:UPI0000165A9E; GB:AE007317; PIDN:AAL00436.1;
C;Genetics:
A;Gene: trpF
C;Superfamily: phosphoribosylanthranilate isomerase; trpF homology
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 54.8%; Score 34; DB 2; Length 209;
Best Local Similarity 36.4%; Pred. No. 83;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
| ||| : ||
Db 7 RSCRLTKVKIC 17

RESULT 22
S55614
hypothetical protein 20 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55614
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55614
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-237 <TEL>
A;Cross-references: UNIPROT:Q66623; UNIPARC:UPI00000F9D62; GB:U20824; NID:G695172; PIDN:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C;Superfamily: varicella-zoster virus gene 35 protein

Query Match 54.8%; Score 34; DB 2; Length 237;
Best Local Similarity 45.5%; Pred. No. 92;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
| ||| : ||
Db 84 RLCYIIELKTC 94

RESULT 23
AI3176

transcription regulator, AraC family attO [imported] - Agrobacterium tumefaciens (strain C); Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: A13176
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: A13176
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-254 <KUR>
 A;Cross-references: UNIPROT:Q8UKG8; UNIPARC:UPI00000D14FC; GB:AE008687; PIDN:AAL45831.1;
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: attO
 A;Genome: plasmid

Query Match 54.8%; Score 34; DB 2; Length 254;
 Best Local Similarity 50.0%; Pred. No. 97;
 Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVCR 12

Db 123 RLCEIIVVLAIR 134

RESULT 24

H84684
 En/Spm-like transposon protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: H84684
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.B.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: H84684
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-268 <STO>
 A;Cross-references: UNIPROT:Q9SKM6; UNIPARC:UPI00000AA595; GB:AE002093; NID:G4432833; PI
 C;Genetics:
 A;Gene: At2g28440
 A;Map position: 2

Query Match 54.8%; Score 34; DB 2; Length 268;
 Best Local Similarity 45.5%; Pred. No. 1e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVC 11

Db 4 KLCEIVMLSIC 14

RESULT 25

G protein-coupled receptor homolog [imported] - human herpesvirus 6
 C;Species: human herpesvirus 6
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T44011; T44198
 R;Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa
 J. Virol. 73, 8053-8063, 1999
 A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
 A;Reference number: 222732; MUID:99412319; PMID:10482554
 A;Accession: T44011
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
 A;Residues: 1-301 <ISE>
 A;Cross-references: UNIPROT:P52542; UNIPARC:UPI00000008F4; EMBL:AB021506; NID:G4995977; I
 A;Experimental source: strain HST; pop. variant B
 R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
 J. Virol. 73, 8040-8052, 1999
 A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
 A;Reference number: 222734; MUID:99412318; PMID:10482553
 A;Accession: T44198
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-301 <DOM>
 A;Cross-references: UNIPARC:UPI00000008F4; EMBL:AF157706; PIDN:AAB06349.1
 A;Experimental source: strain 229; variant B
 C;Genetics:
 A;Gene: US1

Query Match 54.8%; Score 34; DB 2; Length 301;
 Best Local Similarity 41.7%; Pred. No. 1.1e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVCR 12

Db 268 RLCSILVNLCK 279

RESULT 26

T33205
 hypothetical protein ZK6.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Oct-2004
 C;Accession: T33205
 R;Wu, X.
 submitted to the EMBL Data Library, May 1998
 A;Description: The sequence of C. elegans cosmid ZK6.
 A;Reference number: Z21301
 A;Accession: T33205
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-310 <WUX>
 A;Cross-references: UNIPARC:UPI000017A1B6; EMBL:AF067942; PIDN:AAC17689.1; GSPDB:GN00023;
 A;Experimental source: strain Bristol N2; clone ZK6
 C;Genetics:
 A;Gene: CESP:ZK6.1
 A;Map position: 5
 A;Introns: 72/1; 107/2; 224/1

Query Match 54.8%; Score 34; DB 2; Length 310;
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVIRV 10

Db 50 RYCRITVCRV 59

RESULT 27

H81064
 sensor histidine kinase NMB1606 [imported] - Neisseria meningitidis (strain MCS8 serogro
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: H81064
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: H81064
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-505 <TET>

A;Cross-references: UNIPROT:Q9JYF5; UNIPARC:UPI00000C4753; GB:A5002511; GB:A5002098; NID:
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1606

Query Match 54.8%; Score 34; DB 2; Length 505;
Best Local Similarity 41.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LRCRIVVIRVC 12
:|:|:|:|:
Db 353 KLCKIIDGNICR 364

RESULT 28
P2MWB

2a protein - broad bean mottle virus
C;Species: broad bean mottle virus
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A42453
R;Romero, J.; Dziaanott, A.M.; Bujarski, J.J.
Virology 187, 671-681, 1992
A;Title: The nucleotide sequence and genome organization of the RNA2 and RNA3 segments
A;Reference number: A42453; MUID:92188542; PMID:1546462
A;Accession: A42453
A;Molecule type: Genomic RNA
A;Residues: 1-810 <ROM>
A;Cross-references: UNIPROT:P27462; UNIPARC:UPI0000137FE4; GB:M64713; NID:g210666; PIDN:
C;Comment: This protein is a trans-acting factor in viral RNA replication.
C;Genetics:
A;Map position: segment 2
C;Superfamily: alfalfa mosaic virus 90K protein
C;Keywords: nonstructural protein; RNA replication

Query Match 54.8%; Score 34; DB 1; Length 810;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 12
:|:|:|:|:
Db 667 LCRILTALKYCK 677

RESULT 29
T50247

probable helicase [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50247
R;Aert, R.; Voickaert, G.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z25049
A;Accession: T50247
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1717 <AER>
A;Cross-references: UNIPROT:Q9P7T8; UNIPARC:UPI000006B0E1; EMBL:AL138666; PIDN:CAB71840.
A;Experimental source: strain 972h(-); cosmid c694
C;Genetics:
A;Gene: SPDB:SPAC694.02
A;Map position: 1

Query Match 54.8%; Score 34; DB 2; Length 1717;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 11
:|:|:|:|:
Db 264 LCKLILITC 273

RESULT 30
.G86225

hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86225
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86225
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-550 <STO>
A;Cross-references: UNIPROT:O80479; UNIPARC:UPI00000A3848; GB:A5005172; NID:g3249095; PID:
C;Genetics:
A;Map position: 1

Query Match 54.0%; Score 33.5; DB 2; Length 550;
Best Local Similarity 63.6%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LRCRIVVIRVC 11
:|:|:|:|:
Db 269 LRCRMLVL-VC 278

RESULT 31
B82903

hypothetical protein U0341 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: B82903
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A;Reference number: A82870
A;Accession: B82903
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <GLA>
A;Cross-references: UNIPARC:UPI00000C1C28; GB:AE002131; GB:AF222894; NID:g6899316; PIDN:;
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: U0341
A;Genetic code: SGC3

Query Match 53.2%; Score 33; DB 2; Length 191;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 11
:|:|:|:|:
Db 173 LCLLVIIIC 182

RESULT 32
S35292

hypothetical protein 0.0 - Yersinia enterocolitica (fragment)
C;Species: Yersinia enterocolitica
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: S35292; S28575
R;Zhang, L.; Al-Hendy, A.; Toivanen, P.; Skurnik, M.
Mol. Microbiol. 9, 309-321, 1993
A;Title: Genetic organization and sequence of the rfb gene cluster of Yersinia enterocoli
polysaccharide transport systems.
A;Reference number: S35292; MUID:94018626; PMID:7692217
A;Accession: S35292

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-200 <ZHA>
A;Cross-references: UNIPROT:Q56898; UNIPARC:UPI00000B2206; EMBL:Z18920; NID:948582; PIDN
C;Superfamily: Naphthoate synthase; enoyl-CoA hydratase homology
F;24-175/Domain: enoyl-CoA hydratase homology <ECH>
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992

Query Match 53.2%; Score 33; DB 2; Length 200;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
|||:|:
Db 109 CRVIVFCIC 117

RESULT 33
F69937
conserved hypothetical protein ypjG - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69937
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerxon, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
teck, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holbappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69937
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-224 <KUN>
A;Cross-references: UNIPROT:P42981; UNIPARC:UPI0000060638; GB:Z99115; GB:AL009126; NID:9
A;Experimental source: strain 168
C;Genetics:
A;Gene: ypjG

Query Match 53.2%; Score 33; DB 2; Length 224;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 IVVIRVCR 12
:|::|:
Db 90 VTVVIRICR 97

RESULT 34
H69454
enoyl-CoA hydratase (fad-4) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: H69454
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69454
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-254 <KLE>
A;Cross-references: UNIPROT:Q28632; UNIPARC:UPI0000056C43; GB:AE000989; GB:AE000782; NID:
C;Superfamily: Naphthoate synthase; enoyl-CoA hydratase homology
F;24-175/Domain: enoyl-CoA hydratase homology <ECH>
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992

Query Match 53.2%; Score 33; DB 1; Length 254;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLCRIVVIR 9
|||:|:
Db 45 RLVRVVVIR 53

RESULT 35
AH2432
hypothetical protein all5016 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2432
R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2432
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 <KUR>
A;Cross-references: UNIPROT:Q8YMB9; UNIPARC:UPI00000CED25; GB:BA000019; PIDN:BA076715.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all5016

Query Match 53.2%; Score 33; DB 2; Length 273;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CRIVVIR 9
|||:|:
Db 263 CRVVVVR 269

RESULT 36
B81599
hypothetical protein CP0236 [imported] - Chlamydia pneumoniae (strain AR39)
C;Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81599
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, I
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: AB1500; MUID:20150255; PMID:10684935
A;Accession: B81599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <REA>
A;Cross-references: UNIPROT:Q9K2B7; UNIPARC:UPI00000CCC4B; GB:AE002184; GB:AE002161; NID:
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0236
C;Superfamily: Chlamydia pneumoniae hypothetical protein CP0236

Query Match 53.2%; Score 33; DB 2; Length 279;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 11
|||:|:
Db 43 LCALLIILVC 52

```
RESULT 37
A86555
hypothetical protein CPJ0517 [imported] - Chlamydothila pneumoniae (strain J138)
C;Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86555
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishiguro, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: A86555
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <STO>
A;Cross-references: UNIPROT:Q92835; UNIPARC:UPI00000470F3; GB:BA000008; NID:58978887; PMID:10871362
C;Genetics:
C;Superfamily: Chlamydia pneumoniae hypothetical protein CP0236
A;Gene: CPJ0517
Query Match 53.2%; Score 33; DB 2; Length 279;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 LCRIVIRVC 11
|| :|||
Db 43 LCALLIILVC 52
|| :|||

RESULT 38
C72070
hypothetical protein CP0236 [imported] - Chlamydothila pneumoniae (strain CWL029)
C;Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: C72070
R;Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: C72070
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <ARN>
A;Cross-references: UNIPROT:Q92835; UNIPARC:UPI00000470F3; GB:AE001636; NID:10192388
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: CPN0517
C;Superfamily: Chlamydia pneumoniae hypothetical protein CP0236
Query Match 53.2%; Score 33; DB 2; Length 279;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 LCRIVIRVC 11
|| :|||
Db 43 LCALLIILVC 52
|| :|||

RESULT 39
T47475
hypothetical protein F18N11.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47475
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.
submitted to the Protein Sequence Database, February 2000
A;Reference number: 224467
A;Accession: T47475
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-291 <TOR>
A;Cross-references: UNIPROT:Q9M3E3; UNIPARC:UPI000000A2BCD; EMBL:AL132953
```

A;Experimental source: cultivar Columbia; BAC clone F18N11

C;Genetics:

A;Map position: 3

A;Introns: 50/2; 102/3; 195/1; 220/2

A;Note: F18N11.110

Query Match 53.2%; Score 33; DB 2; Length 291;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 2 LC-RIVIRVC 11

|| :|||

Db 243 LCTPRIVVILVC 254

RESULT 40

AB3057

conserved hypothetical protein Atu4071 [imported] - Agrobacterium tumefaciens (strain C58)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 06-Jan-2003

C;Accession: AB3057

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

exage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan,

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AB3057

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-346 <XUR>

A;Cross-references: UNIPARC:UPI00000D2428; GB:AE008689; PIDN:AAL44872.1; PID:gl17742520; C

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu4071

A;Map position: linear chromosome

C;Superfamily: uncharacterized conserved protein

Query Match 53.2%; Score 33; DB 2; Length 346;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIVIRVC 12

|||||

Db 27 RLCRAVAARLDR 38

RESULT 41

D98229

hypothetical protein AGR L1570 [imported] - Agrobacterium tumefaciens (strain C58, Cerec

C;Species: Agrobacterium tumefaciens

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 06-Jan-2003

C;Accession: D98229

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: D98229

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-346 <XUR>

A;Cross-references: UNIPARC:UPI00000D2428; GB:AE007870; PIDN:AAK89358.1; PID:gl15159206; C

C;Genetics:

A;Gene: AGR_L_1570

A;Map position: linear chromosome

C;Superfamily: uncharacterized conserved protein

Query Match 53.2%; Score 33; DB 2; Length 346;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy      1 RLCRIWIRVCR 12
      ||||| | | | |
Db      27 RLCRAVAARLDR 38
      ||||| | | | |

RESULT 42
T29843
hypothetical protein W02D7.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29843
R:Du, Z.; Le, T.T.
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-349 <DUZ>
A:Cross-references: UNIPROT:O17527; UNIPARC:UPI000017BC13; EMBL:AF014940; PIDN:AAB63936
A:Experimental source: strain Bristol N2; clone W02D7
C:Genetics:
A:Gene: CESP:W02D7.6
A:Map position: 5
A:Introns: 121/3; 195/3; 291/2; 324/2

Query Match      53.2%; Score 33; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      4 RIVIRVCR 12
      ||||| | | | |
Db      220 RIVIRVCR 228
      ||||| | | | |

RESULT 43
A56856
retinoid-related orphan receptor RZR-alpha - human
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 31-Dec-2004
C:Accession: A56856; I52276
R:Carlberg, C.; van Huijduijnen, R.H.; Staple, J.K.; DeLamarter, J.F.; Becker-Andre, M.
Mol. Endocrinol. 8, 757-770, 1994
A:Title: RZRs, a new family of retinoid-related orphan receptors that function as both m
A:Reference number: A56856; MUID:95021307; PMID:7935491
A:Accession: A56856
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-468 <CAR>
A:Cross-references: UNIPARC:UPI000016AFE2; GB:L14611; NID:G348240; PIDN:AAA02963.1; PID:
A:Note: authors translated the codon ATT for residue 443 as Met
R:Becker-Andre, M.; Andre, E.; DeLamarter, J.F.
Biochem. Biophys. Res. Commun. 194, 1371-1379, 1993
A:Title: Identification of nuclear receptor mRNAs by RT-PCR amplification of conserved z
A:Reference number: I52276; MUID:93356815; PMID:7916608
A:Accession: I52276
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-468 <RES>
A:Cross-references: UNIPARC:UPI000016AFE2; GB:L14611; NID:G348240; PIDN:AAA02963.1; PID:
C:Keywords: DNA binding; transcription factor; zinc finger
F:16-376/Domain: erba transforming protein homology <ERBA>

Query Match      53.2%; Score 33; DB 2; Length 468;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5 IVIRVCR 12
      ||||| | | | |
Db      308 VVIRVCR 315
      ||||| | | | |
```

```
RESULT 44
B56182
fibroblast growth factor receptor 2 isoform IIIC - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 19-Oct-1995 #sequence_revision 19-Jan-1996 #text_change 16-Jul-1999
C:Accession: B56182
R:Mathieu, M.; Kiefer, P.; Mason, I.; Dickson, C.
J. Biol. Chem. 270, 6779-6787, 1995
A:Title: Fibroblast growth factor (FGF) 3 from Xenopus laevis (XFGF3) binds with high afi
A:Reference number: A56182; MUID:95204476; PMID:7896824
A:Accession: B56182
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-480 <MAT>
A:Cross-references: UNIPARC:UPI00000FD731
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C:Keywords: growth factor receptor
F:183-244/Domain: immunoglobulin homology <IMM>

Query Match      53.2%; Score 33; DB 2; Length 480;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      3 CRIVVIRVCR 12
      ||||| | | | |
Db      401 CMVVVVCVCR 410
      ||||| | | | |

RESULT 45
A56182
fibroblast growth factor receptor 2 isoform IIB - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 19-Oct-1995 #sequence_revision 19-Jan-1996 #text_change 16-Jul-1999
C:Accession: A56182
R:Mathieu, M.; Kiefer, P.; Mason, I.; Dickson, C.
J. Biol. Chem. 270, 6779-6787, 1995
A:Title: Fibroblast growth factor (FGF) 3 from Xenopus laevis (XFGF3) binds with high afi
A:Reference number: A56182; MUID:95204476; PMID:7896824
A:Accession: A56182
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-480 <MAT>
A:Cross-references: UNIPARC:UPI00000FBF64
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C:Keywords: growth factor receptor
F:183-244/Domain: immunoglobulin homology <IMM>

Query Match      53.2%; Score 33; DB 2; Length 480;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      3 CRIVVIRVCR 12
      ||||| | | | |
Db      401 CMVVVVCVCR 410
      ||||| | | | |

RESULT 46
T08539
hypothetical protein F27B13.20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08539
R:Bevan, M.; Zimmermann, W.; Grueniseisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Maye
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16442
A:Accession: T08539
A:Molecule type: DNA
A:Residues: 1-515 <BEV>
A:Cross-references: UNIPROT:Q9SZQ1; UNIPARC:UPI000000AACFA; EMBL:AL050352; GSPDB:GN000062;
A:Experimental source: cultivar Columbia; BAC clone F27B13
C:Genetics:
A:Gene: ATSP:F27B13.20
A:Map position: 4
```

C;Superfamily: Arabidopsis thaliana hypothetical protein F27B13.20

Query Match 53.2%; Score 33; DB 2; Length 515;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CRIVVIRVCR 12
 | : || |||
Db 254 CHKLIVIEVCR 263

RESULT 47

T12094

beta-fructofuranosidase (EC 3.2.1.26) - fava bean

C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T12094

R;Weber, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus, U.

Plant Cell 7, 1835-1846, 1995

A;Title: Seed coat-associated invertases of Fava bean control both unloading and storage

A;Reference number: Z17416; MUID:96093423; PMID:8535137

A;Accession: T12094

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-575 <WEB>

A;Cross-references: UNIPROT:Q43855; UNIPARC:UPI000009D74A; EMBL:Z35162; NID:9861154; PID

A;Experimental source: cv. Fribo, seed coat

C;Genetics:

A;Gene: CWINV1

C;Superfamily: beta-fructofuranosidase

C;Keywords: cell wall; glycoprotein; glycosidase; hydrolase

Query Match 53.2%; Score 33; DB 2; Length 575;

Best Local Similarity 70.0%; Pred. No. 2.8e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LCRIVVIRVC 11
 | | | | |
Db 8 LCLIVFILVC 17

RESULT 48

T05425

polyadenylate-binding protein F28A23.130 - Arabidopsis thaliana

N;Alternate names: poly(A)-binding protein

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05425

R;Bavan, M.; Weichselgartner, M.; Partmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; N

submitted to the Protein Sequence Database, October 1998

A;Reference number: Z15415

A;Accession: T05425

A;Molecule type: DNA

A;Residues: 1-629 <BEV>

A;Cross-references: UNIPROT:P42731; UNIPARC:UPI000000BD7E; EMBL:AL021961

A;Experimental source: cultivar Columbia; BAC clone F28A23

C;Genetics:

A;Map position: 4

A;Introns: 90/1; 129/2; 348/3; 374/3; 404/3; 450/3; 507/3; 557/3

A;Note: F28A23.130

C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

C;Keywords: nucleus; RNA binding

F;216-282/Domain: ribonucleoprotein repeat homology <RRM>

Query Match

Best Local Similarity 53.2%; Score 33; DB 2; Length 629;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVVIRVCR 12
 | : || |||
Db 62 VVTVRVCR 69

RESULT 49

S37085

polyadenylate-binding protein - fern (Anemia phyllitidis)

C;Species: Anemia phyllitidis

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S37085

R;Yugrek, O.; Moepps, B.; Schraudolph, H.

submitted to the EMBL Data Library, September 1993

A;Description: Molecular identification of a cDNA encoding the poly(A)-binding protein ir

A;Reference number: S37085

A;Accession: S37085

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <VUG>

A;Cross-references: UNIPROT:Q39953; UNIPARC:UPI000000ACFE; EMBL:Z26042; NID:9398326; PID

C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

F;27-94/Domain: ribonucleoprotein repeat homology <RRM1>

F;115-181/Domain: ribonucleoprotein repeat homology <RRM2>

F;205-271/Domain: ribonucleoprotein repeat homology <RRM3>

F;308-374/Domain: ribonucleoprotein repeat homology <RRM4>

Query Match 53.2%; Score 33; DB 2; Length 638;

Best Local Similarity 66.7%; Pred. No. 3e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RIVVIRVCR 12
 | : | ||||
Db 51 QVVSVIRVCR 59

RESULT 50

B70396

histidine kinase sensor protein - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: B70396

R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Graham, D.E.; Ove

V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: B70396

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-646 <AQF>

A;Cross-references: UNIPROT:O67197; UNIPARC:UPI00000056527; GB:AE000724; NID:92983585; PII

A;Experimental source: strain VF5

C;Genetics:

A;Gene: hksP1

Query Match 53.2%; Score 33; DB 2; Length 646;

Best Local Similarity 55.6%; Pred. No. 3.1e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVVIRV 10
 | | | | |
Db 263 LCLIIIRI 271

RESULT 51

H95852

hypothetical fusion protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmaic

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 31-Dec-2004

C;Accession: H95852

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasamid from the N2-fixing endos

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: H95852

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-658 <KUR>

A;Cross-references: UNIPROT:Q92X74; UNIPARC:UPI0000003B3E6; GB:AL591985; PIDN:CAC48488.1;
 R;Experimental source: strain 1021, megaplasmid pSYMB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: SMD20088
 A;Genome: plasmid
 C;Superfamily: uncharacterized conserved protein with erythromycin esterase domain

Query Match 53.2%; Score 33; DB 2; Length 658;
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LCRIVIRVCR 12
 Db 415 RKCEAVVRQCR 426

RESULT 52
 A49123
 fibroblast growth factor receptor 2 precursor - African clawed frog
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C;Species: *Xenopus laevis* (African clawed frog)
 C;Date: 21-Jan-1994 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
 C;Accession: A49123; S25060
 R;Friesel, R.; Brown, S.A.
 Development 116, 1051-1058, 1992
 A;Title: Spatially restricted expression of fibroblast growth factor receptor-2 during x
 A;Reference number: A49123; MUID:93201992; PMID:1284237
 A;Accession: A49123
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-813 <FRI>
 A;Cross-references: UNIPROT:Q03364; UNIPARC:UPI0000172603; EMBL:X65943
 A;Note: sequence extracted from NCBI backbone (NCBIP:128003)
 R;Brown, S.N.; Friesel, R.E.
 submitted to the EMBL Data Library, May 1992
 A;Description: *Xenopus* fibroblast growth factor receptor-2: cloning, expression and deve
 A;Reference number: S25060
 A;Accession: S25060
 A;Molecule type: mRNA
 A;Residues: 1-632, 'A', 634-813 <BRO>
 A;Cross-references: UNIPARC:UPI000012A72B; EMBL:X65943; NID:964694; PIDN:CAA46758.1; PID
 C;Function:
 A;Description: receptor mediating fibroblast growth factor roles in patterning of develo
 A;Note: expressed from embryonic stage 11 through tadpole stages
 C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
 C;Keywords: ATP; autophosphorylation; duplication; embryo; glycoprotein; growth factor

F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-813/Product: fibroblast growth factor receptor 2 #status predicted <MAT>
 F;18-367/Domain: extracellular #status predicted <EXT>
 F;124-130/Region: acidic
 F;163-223/Domain: immunoglobulin homology <IMM>
 F;368-388/Domain: transmembrane #status predicted <TM>
 F;389-813/Domain: intracellular #status predicted <INT>
 F;469-754/Domain: protein kinase homology <KIN>
 F;477-485/Region: protein kinase ATP-binding motif
 F;58-103,170-221,268-332/Disulfide bonds: #status predicted
 F;79,115,231,255,287,308,321/Binding site: carbohydrate (Asn) (covalent) #status predict
 F;507,524,616/Active site: Lys, Glu, Asp #status predicted
 F;621,634/Binding site: magnesium (Asn, Asp) #status predicted
 F;647/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 53.2%; Score 33; DB 1; Length 813;
 Best Local Similarity 60.0%; Pred. No. 3.7e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 CRIVIRVCR 12
 Db 380 CMVVVVCVCR 389

RESULT 53
 T04492
 protein kinase homolog F8F16.70 - Arabidopsis thaliana
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 31-Dec-2004
 C;Accession: T04492
 R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hobeisel, J.; Mewes
 submitted to the Protein Sequence Database, April 1998
 A;Reference number: Z15375
 A;Accession: T04492
 A;Molecule type: DNA
 A;Residues: 1-951 <BEV>
 A;Cross-references: UNIPROT:O49575; UNIPARC:UPI0000048A36; EMBL:AL021633
 A;Experimental source: cultivar Columbia; BAC clone F8F16
 C;Genetics:
 A;Map position: 4
 A;Introns: 224/1; 461/1; 684/2; 703/2; 729/3; 744/1; 806/2
 A;Note: F8F16.70
 C;Superfamily: Receptor-like protein kinase

Query Match 53.2%; Score 33; DB 2; Length 951;
 Best Local Similarity 45.5%; Pred. No. 4.2e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 12
 Db 799 LCKLTSIRPCK 809

RESULT 54
 T47605
 RING finger-like protein - Arabidopsis thaliana
 N;Alternate names: protein T14E10.30
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: T47605
 R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke, K.; M
 submitted to the Protein Sequence Database, March 2000
 A;Reference number: Z24463
 A;Accession: T47605
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1378 <OBE>
 A;Cross-references: UNIPROT:Q9M111; UNIPARC:UPI0000000C34A; EMBL:AL138656
 A;Experimental source: cultivar Columbia; BAC clone T14E10
 C;Genetics:
 A;Map position: 3
 A;Introns: 199/2; 1050/2; 1121/3; 1212/3; 1232/3; 1276/2; 1314/3
 A;Note: T14E10.30

Query Match 53.2%; Score 33; DB 2; Length 1378;
 Best Local Similarity 60.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CRIVIRVCR 12
 Db 1055 CRLPVITPCR 1064

RESULT 55
 S43417
 RNA/DNA-binding protein - mouse
 C;Species: *Mus musculus* (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
 C;Accession: S43417
 R;Schmidt, G.; Werner, D.

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Biochim. Biophys. Acta 1216, 317-320, 1993
A;Title: Sequence of a complete murine cDNA reflecting an S phase-prevalent transcript e
A;Reference number: S43417; MUID:94060110; PMID:8241277
A;Accession: S43417
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-365 <SCH>
A;Cross-references: UNIPROT:Q62150; UNIPARC:UPI000002891B; EMBL:X70067; NID:9433436; PID
F;161-229/Domain: ribonucleoprotein repeat homology <BRM2>

Query Match 52.4%; Score 32.5; DB 2; Length 365;
Best Local Similarity 46.7%; Pred. No. 2.4e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 RLCRIV---VIRVC 12
||| : : : |||
Db 320 RLCFVLFFSSQVRVC 334

RESULT 56
QOBE35
BRRF3 protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C;Accession: G43043; A03777; S3030
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: G43043
A;Molecule type: DNA
A;Residues: 1-405 <GAN>
A;Cross-references: UNIPROT:P03215; UNIPARC:UPI000000CDB4; EMBL:V01555; NID:959074; PIDN
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: cytomegalovirus UL100 protein

Query Match 52.4%; Score 32.5; DB 1; Length 405;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 2 LCRI-VVIRVC 12
|| : : : |||
Db 313 LCSVAMLRIC 324

RESULT 57
T02657
hypothetical protein F12C20.18 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02657
R;Rounsley, S.D.; Ronning, C.M.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence.
A;Reference number: Z14685
A;Accession: T02657
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-954 <ROU>
A;Cross-references: UNIPROT:Q8S8S6; UNIPARC:UPI000017AF66; EMBL:AC005168; NID:93426033;
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 2
A;Introns: 112/3; 168/3; 266/3; 325/3; 413/3; 455/3; 517/2; 629/2; 674/2; 682/3; 738/3;
A;Note: F12C20.18

Query Match 52.4%; Score 32.5; DB 2; Length 954;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

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QY 1 RLCRIV---VIRVC 11
||| : : : |||
Db 354 KLCRAVTSLTIRIC 367

RESULT 58
G84664
hypothetical protein At2g26780 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84664
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; A
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
eusa, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84664
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1732 <STO>
A;Cross-references: UNIPROT:Q8S8S6; UNIPARC:UPI00000A3C05; GB:AE002093; NID:96598445; PFI
C;Genetics:
A;Gene: At2g26780
A;Map position: 2

Query Match 52.4%; Score 32.5; DB 2; Length 1732;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 RLCRIV---VIRVC 11
||| : : : |||
Db 1132 KLCRAVTSLTIRIC 1145

RESULT 59
T25554
hypothetical protein C17H11.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25554
R;Johnson, D.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid C17H11.
A;Reference number: Z20049
A;Accession: T25554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-112 <JOH>
A;Cross-references: UNIPROT:P91066; UNIPARC:UPI0000077BA4; EMBL:U80847; PIDN:AAB37986.1;
A;Experimental source: strain Bristol N2; clone C17H11
C;Genetics:
A;Gene: CESP:C17H11.5
A;Map position: X
A;Introns: 34/2; 58/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C17H11.5

Query Match 51.6%; Score 32; DB 2; Length 112;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVC 12
|| : : : |||
Db 77 RPNVNVIRFICR 88

RESULT 60
T07522
ribosomal protein L14 - Japanese black pine chloroplast
C;Species: chloroplast Pinus thunbergiana (Japanese black pine)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07522

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R;Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudaaki, T.; Sugiura, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
 A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
 A;Reference number: Z16030; MUID:95024047; PMID:7937893
 A;Accession: T07522
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-122 <WAK>
 A;Cross-references: UNIPROT:P41633; UNIPARC:UPI00001339F4; EMBL:DI7510; NID:G529643; PID
 C;Genetics:
 A;Gene: rpl14
 A;Genome: chloroplast
 A;Superfamily: ribosomal protein L14/L17/L23
 C;Keywords: chloroplast; ribosome

Query Match 51.6%; Score 32; DB 2; Length 122;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RIVWVRCR 12
 |||||
 Db 59 RAVVIRTC 67

RESULT 61
 F75337
 transposase - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: F75337
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: F75337
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-145 <WHI>
 A;Cross-references: UNIPROT:Q9RT39; UNIPARC:UPI00000D7386; GB:AE002032; GB:AE000513; NID
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR1927
 A;Map position: 1
 C;Superfamily: conserved hypothetical protein 4 (insertion sequence ISH1.8)

Query Match 51.6%; Score 32; DB 2; Length 145;
 Best Local Similarity 40.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVWVRCR 12
 |||||
 Db 37 CRELLIQICK 46

RESULT 62
 S31078
 seed allergen RA5 - rice
 C;Species: Oryza sativa (rice)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
 C;Accession: S31078
 R;Adachi, T.; Izumi, H.; Yamada, T.; Tanaka, K.; Takeuchi, S.; Nakamura, R.; Matsuda, T.
 Plant Mol. Biol. 21, 239-248, 1993
 A;Title: Gene structure and expression of rice seed allergenic proteins belonging to the
 A;Reference number: S31078; MUID:93144699; PMID:7678765
 A;Accession: S31078
 A;Molecule type: mRNA
 A;Residues: 1-157 <ADA>
 A;Cross-references: UNIPROT:Q01881; UNIPARC:UPI000013300A; EMBL:DI1430; NID:G218196; PID
 C;Keywords: seed

Query Match 51.6%; Score 32; DB 2; Length 157;

Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CRIVWVRCR 12
 |||||
 Db 55 CRALVRCR 64

RESULT 63
 AC0883
 conserved hypothetical protein STY3300 [imported] - Salmonella enterica subsp. enterica
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AC0883
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AC0883
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-161 <PAR>
 A;Cross-references: UNIPARC:UPI000005R462; GB:AL513382; PIDN:CAD02963.1; PID:G16504211; C
 C;Genetics:
 A;Gene: STY3300

Query Match 51.6%; Score 32; DB 2; Length 161;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RLCRIVWVRCR 12
 |||||
 Db 77 RLRTAVLTCCR 88

RESULT 64
 AB2644
 flagellar protein FLGA precursor [imported] - Agrobacterium tumefaciens (strain C58, Dup
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AB2644
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AB2644
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-162 <KUR>
 A;Cross-references: UNIPROT:Q44339; UNIPARC:UPI000012A8EE; GB:AE008688; PIDN:AAL41568.1;
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: flga
 A;Map position: circular chromosome
 C;Superfamily: flagellar protein FLGA precursor

Query Match 51.6%; Score 32; DB 2; Length 162;
 Best Local Similarity 44.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVWVRCR 11
 |||||
 Db 10 CRTALVRMC 18

RESULT 65

T12510
hypothetical protein DKFp434F22.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12510
R;Ansoerge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17527
A;Accession: T12510
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-220 <ANS>
A;Cross-references: UNIPROT:Q9Y4MG; UNIPARC:UPI000006B004; EMBL:AL080203
A;Experimental source: adult testis; clone DKFp434F222
C;Genetics:
A;Note: DKFp434F22.1
C;Superfamily: DNA-directed DNA polymerase II

Query Match 51.6%; Score 32; DB 2; Length 220;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 3 CRIVV--IRVCR 12
|||::||:|
Db 139 CRVVHGVQACR 150

RESULT 66

AC2825
transcription regulator Atu2025 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AC2825
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-226 <KUR>
A;Cross-references: UNIPROT:Q8UDU4; UNIPARC:UPI0000164690; GB:AE008688; PIDN:AAL43017.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2025
A;Map position: circular chromosome

Query Match 51.6%; Score 32; DB 2; Length 226;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RIVVIRVCR 12
|::|||
Db 76 RMAVINVCR 84

RESULT 67

B97603
hypothetical protein AGR_C3670 [imported] - Agrobacterium tumefaciens (strain C58, Cere)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97603
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97603

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 <KUR>
A;Cross-references: UNIPROT:Q8UDU4; UNIPARC:UPI00000D1D5F; GB:AE007869; PIDN:AAK87779.1;
C;Genetics:
A;Gene: AGR_C3670
A;Map position: circular chromosome

Query Match 51.6%; Score 32; DB 2; Length 231;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RIVVIRVCR 12
|::|||
Db 81 RMAVINVCR 89

RESULT 68

D75362
Far-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: D75362
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75362
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <WHI>
A;Cross-references: UNIPROT:Q9RTPO; UNIPARC:UPI00000D3EC1; GB:AE002013; GB:AE000513; NID:
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRI17
A;Map position: 1

Query Match 51.6%; Score 32; DB 2; Length 274;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLCRIVVI 8
|||::|
Db 110 RLCRVTVI 117

RESULT 69

T27597
hypothetical protein ZC47.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27597
R;McMurray, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20391
A;Accession: T27597
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-277 <WIL>
A;Cross-references: UNIPROT:P92151; UNIPARC:UPI000007C541; EMBL:Z81141; PIDN:CAB03495.1;
A;Experimental source: clone ZC47
C;Genetics:
A;Gene: CESP:ZC47.7
A;Introns: 23/2; 212/3

Query Match 51.6%; Score 32; DB 2; Length 277;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RIVVIRVCR 12
|::|||

Db 23 RLAVRKVC 31

RESULT 70

hypothetical protein ZK1037.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T27662

R:Baaham, V.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z20401

A:Accession: T27662

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-338 <WIL>

A:Cross-references: UNIPROT:Q45989; UNIPARC:UPI0000061344; EMBL:Z81142; PIDN:CAB03506.1

C:Genetics:

A:Gene: CESP:ZK1037.7

A:Map position: 5

A:Introns: 24/2; 77/2; 170/2; 246/2

Query Match 51.6%; Score 32; DB 2; Length 338;

Best Local Similarity 62.5%; Pred. No. 2.8e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ILVIRVC 12

Db 222 ILVIRICK 229

RESULT 71

C72711

hypothetical protein APE1106 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: C72711

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999

A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: C72711

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-350 <KAW>

A:Cross-references: UNIPROT:Q9YD06; UNIPARC:UPI000005DDF8; DDBJ:AP0000060; NID:g5104188;

C:Genetics:

A:Gene: APE1106

C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1557

Query Match 51.6%; Score 32; DB 2; Length 350;

Best Local Similarity 60.0%; Pred. No. 2.8e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 12

Db 318 CRVEVRVC 327

RESULT 72

T05427

hypothetical protein F28A23.150 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T05427

R:Bevan, M.; Weischelgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; Nsubmitted to the Protein Sequence Database, October 1998

A:Reference number: Z15415

A:Accession: T05427

A:Molecule type: DNA

A:Residues: 1-377 <BEV>

A:Cross-references: UNIPROT:Q49495; UNIPARC:UPI000009E2B7; EMBL:AL021961

A:Experimental source: cultivar Columbia; BAC clone F28A23

C:Genetics:

A:Map position: 4

A:Introns: 99/1; 127/1; 152/1; 166/2; 185/3; 220/1; 235/3; 267/2; 294/3

A:Note: F28A23.150

Query Match 51.6%; Score 32; DB 2; Length 377;

Best Local Similarity 66.7%; Pred. No. 3e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11

Db 43 CRIVIVDC 51

RESULT 73

T21367

hypothetical protein F25H8.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21367

R:Gajadaty, S.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19413

A:Accession: T21367

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-390 <WIL>

A:Cross-references: UNIPROT:Q19788; UNIPARC:UPI000007A817; EMBL:Z69360; PIDN:CAA93283.1;

A:Experimental source: clone F25H8

C:Genetics:

A:Gene: CESP:F25H8.2

A:Map position: 4

A:Introns: 15/3; 142/3; 179/1; 227/3; 309/1

Query Match

51.6%; Score 32; DB 2; Length 390;

Best Local Similarity 44.4%; Pred. No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11

Db 177 CQVVIISTC 185

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Qy      3  CRIWVIRVC 11
      |||:|
Db      105  CEIAIRSC 113

RESULT 75
AF0791
Probable transmembrane transport protein STY2509 [imported] - Salmonella enterica subsp.
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0791
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0791
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <PAR>
A;Cross-references: UNIPARC:UPI00000D008B; GB:AL513382; PIDN:CAD07512.1; PID:g16503505;
C;Genetics:
A;Gene: STY2509

Query Match      51.6%; Score 32; DB 2; Length 396;
Best Local Similarity 36.4%; Pred. No. 3.1e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      2  LCRIVIRVC 12
      |||::|
Db      248  LCYAILMICR 258

RESULT 76
I38603
heme A farnesyltransferase (EC 2.5.1.-) - human
N;Alternate names: cytochrome-c oxidase assembly protein; heme A3 synthetase
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C;Accession: I38603
R;Glerum, M.D.; Izagoloff, A.
Proc. Natl. Acad. Sci. U.S.A. 91, 8452-8456, 1994
A;Title: Isolation of a human cDNA for heme A:farnesyltransferase by functional compleme
A;Reference number: I38603; MUID:94359949; PMID:8078902
A;Accession: I38603
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-443 <RES>
A;Cross-references: UNIPROT:Q12887; UNIPARC:UPI000016A0A5; EMBL:U09466; NID:g495492; PII
C;Genetics:
A;Gene: GDB:COX10
A;Cross-references: GDB:I386460
A;Map position: 17p12-17p11.2
C;Superfamily: COX10 protein
C;Keywords: transferase

Query Match      51.6%; Score 32; DB 2; Length 443;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2  LCRIVIRVC 11
      |||:|
Db      352  LCRVALRHC 361

RESULT 77
B82622
anthranilate synthase component I XF1914 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

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C;Accession: B82622
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-498 <SIM>
A;Cross-references: UNIPROT:Q9PC67; UNIPARC:UPI00000C2895; GB:AE004011; GB:AE003849; NID:
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorrry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
J.D.; Junqueira, M.L.; Kempner, E.L.; Kitajima, J.P.; Marino, C.L.; Marques, M.V.; Martins, E.
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.;
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1914
C;Superfamily: anthranilate synthase component I

Query Match      51.6%; Score 32; DB 2; Length 498;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2  LCRIVIRVC 11
      |||:|
Db      342  LCRNDIVRC 351

RESULT 78
T37840
probable vacuolar protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37840
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21749
A;Accession: T37840
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: DNA
A;Residues: 1-536 <MUR>
A;Cross-references: UNIPROT:O13786; UNIPARC:UPI000006AA47; EMBL:Z99162; PIDN:CAB16219.1;
C;Genetics:
A;Experimental source: strain 972h-; cosmid c17G6
A;Gene: SPDB:SPAC17G6.08
A;Map position: 1
C;Superfamily: vacuolar segregation protein PEP7

Query Match      51.6%; Score 32; DB 2; Length 536;
Best Local Similarity 54.5%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1  RLCRIVIRVC 11
      |||:|
Db      298  RLCGRVICRFC 308

RESULT 79
S70773
cytochrome b245 beta chain - human
N;Alternate names: chronic granulomatous disease protein; X-CGD protein
C;Species: Homo sapiens (man)

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C;Date: 28-Oct-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S70773; A25722; S00462
R;Dinauer, M.C.; Orkin, S.H.; Brown, R.; Jesaitis, A.J.; Parkos, C.A.
Nature 327, 717-720, 1987
A;Title: The glycoprotein encoded by the X-linked chronic granulomatous disease locus is
A;Reference number: S07340; MUID:87258189; PMID:3600768
A;Accession: S70773
A;Molecule type: mRNA
A;Residues: 1-570 <DN>
A;Cross-references: UNIPROT:P04839; UNIPARC:UPI000001628; EMBL:X05895; NID:g30300
A;Note: this is a revision to the sequence from reference A25722
A;Note: Only a list of differences from sequence A25722 is shown
R;Royer-Pokora, B.; Kunkel, L.M.; Monaco, A.P.; Goff, S.C.; Newburger, P.E.; Baehner, R.
Nature 322, 32-38, 1986
A;Title: Cloning the gene for an inherited human disorder--chronic granulomatous disease
A;Reference number: A25722; MUID:86257405; PMID:2425263
A;Accession: A25722
A;Molecule type: mRNA
A;Residues: 103-570 <ROY>
A;Cross-references: UNIPARC:UPI000017C0D6; EMBL:X04011; NID:g37983
A;Note: this sequence has been revised in reference S07340
R;Teahan, C.; Rowe, P.; Parker, P.; Totty, N.; Segal, A.W.
Nature 327, 720-721, 1987
A;Title: The X-linked chronic granulomatous disease gene codes for the beta-chain of cytochrome b590
A;Reference number: S00462; MUID:87258190; PMID:3600769
A;Accession: S00462
A;Molecule type: protein
A;Residues: 2-42, X', 44 <TEA>
A;Cross-references: UNIPARC:UPI0000017C0D7
C;Genetics:
A;Gene: GDB:CYBB; CGD; GP91-PHOX; X-CGD
A;Cross-references: GDB:I20513; OMIM:306400
A;Map position: Xp21.1-Xp21.1
C;Keywords: heterodimer

Query Match 51.6%; Score 32; DB 2; Length 570;
Best Local Similarity 40.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVCR 12
| : : : : |||
Db 64 CMLILLPVCR 73

RESULT 80
T00768
polyadenylate-binding protein T22J18.7 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00768
R;Vyotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Oji, O.; Kwan, A.; Liu, S.; Lititz, D.; Li, X.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N. submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence.
A;Reference number: 214202
A;Accession: T00768
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-655 <VS>
A;Cross-references: UNIPROT:O64380; UNIPARC:UPI000016D899; EMBL:AC003979; NID:g3172156;
C;Genetics:
A;Map position: 1
A;Introns: 102/1; 362/3; 388/3; 418/3; 512/3; 584/3
A;Note: T22J18.7
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
C;Keywords: nucleus; RNA binding
F;137-203/Domain: ribonucleoprotein repeat homology <RRM>

Query Match 51.6%; Score 32; DB 2; Length 655;
Best Local Similarity 45.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVCR 12

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96534
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mai, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C96534
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-671 <STO>
A;Cross-references: UNIPROT:Q9FXA2; UNIPARC:UPI00000A2E97; GB:AE005173; NID:g10120431; P;
C;Genetics:
A;Gene: F14J22.3
A;Map position: 1
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match 51.6%; Score 32; DB 2; Length 671;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RIVVIRVCR 12
| : : : : |||
Db 70 QVSVRVCR 78

RESULT 82
A59348
formate dehydrogenase (EC 1.2.1.2) alpha chain MJ1351 [similarity] - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C;Accession: A59348; H64468
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A59348
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-686 <BUL2>
A;Cross-references: UNIPARC:UPI0000174F62; GB:U67575; GB:L77117; NID:g1591992
A;Note: this ORF is annotated but not translated in GenBank entry U67575, release 117; th authors
A;Note: this ORF is annotated in GenBank entry U67575, release 117 as containing a premat
A;Accession: H64468
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 152-686 <BUL1>
A;Cross-references: UNIPARC:UPI0000174F63; GB:U67575; GB:L77117; NID:g1591992; PID:g159191
A;Note: the original version of GenBank entry U67575, used an incorrect initiation codon
C;Genetics:
A;Gene: MJ1353
C;Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; NAD; F;23,26,30,58/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F;60,145/Active site: Lys, His #status predicted
F;144/Binding site: molybdopterin guanine dinucleotide (Cys) (covalent) #status predicted

F;144/Modified site: selenocysteine #status predicted

Query Match 51.6%; Score 32; DB 2; Length 686;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVWVRC 11
||:| :||
Db 670 LCKIPELKVC 679

RESULT 83

T34182 hypothetical protein C49H3.10 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34182
R;Wu, X.

submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C49H3.

A;Reference number: Z21485
A;Accession: T34182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1175 <WUX>

A;Cross-references: UNIPARC:UPI0000179EE1; EMBL:U42436; PIDN:AAA83487.1; CESP:C49H3.10
C;Genetics:
A;Gene: CESP:C49H3.10
A;Introns: 20/3; 48/2; 145/2; 181/3; 258/3; 298/3; 314/2; 382/2; 439/3; 533/3; 861/1; 10

Query Match 51.6%; Score 32; DB 2; Length 1175;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVWVRC 10
||:| :||
Db 1139 ICRLDVIRV 1147

RESULT 84

T23681 hypothetical protein M02G9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
R;Matthews, L.

submitted to the EMBL Data Library, November 1996
A;Reference number: Z19781

A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-1513 <WIL>

A;Cross-references: UNIPROT:O17970; UNIPARC:UPI0000076B6D; EMBL:Z81573; PIDN:CAB04625.1;
A;Experimental source: clone M02G9

C;Genetics:

A;Gene: CESP:M02G9.1

A;Map position: 2

A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match 51.6%; Score 32; DB 2; Length 1513;
Best Local Similarity 45.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIWVIRVC 11
||:| :||
Db 1163 RVQNVCEVC 1173

RESULT 85

S42373 hypothetical protein T20G5.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004

C;Accession: S42373

R;Smith, A.
submitted to the EMBL Data Library, March 1994

A;Reference number: S42368

A;Accession: S42373

A;Molecule type: DNA

A;Residues: 1-3051 <SMI>

A;Cross-references: UNIPARC:UPI000017BBC8; EMBL:Z30423; NID:g458479; PID:g458485

C;Genetics:

A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1>
F;754-793/Domain: fibronectin type II repeat homology <2F1>
F;1201-1244/Domain: EGF homology <EGF>

Query Match 51.6%; Score 32; DB 2; Length 3051;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIWVIRVC 12
||:| :||
Db 1292 RICRPALVDECR 1303

RESULT 86

A59295

unconventional myosin-15 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C;Accession: A59295

R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; M.J.
an, T.B.; Fridell, R.A.

Genomics 61, 243-258, 1999

A;Title: Characterization of the human and mouse unconventional myosin XV genes responsil
A;Reference number: A59266; MUID:20021762; PMID:10552926

A;Accession: A59295

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-3511 <LIA>

A;Cross-references: UNIPROT:Q9CZZ4; UNIPARC:UPI000002A123; GB:AF144095; NID:g6224684; PII

C;Genetics:

A;Gene: MGI:Myo15

A;Cross-references: MGI:1261811

A;Map position: 11:33.9

F;1209-1871/Domain: myosin motor domain homology <MMO>

Query Match 51.6%; Score 32; DB 2; Length 3511;
Best Local Similarity 55.6%; Pred. No. 1.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVWVRC 10
||:| :||
Db 3482 LCRVAVHV 3490

RESULT 87

A59266

unconventional myosin-15 - human

C;Species: Homo sapiens (man)

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C;Accession: A59266

R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; M.J.

an, T.B.; Fridell, R.A.

Genomics 61, 243-258, 1999

A;Title: Characterization of the human and mouse unconventional myosin XV genes responsil
A;Reference number: A59266; MUID:20021762; PMID:10552926

A;Accession: A59266

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-3530 <LIA>

A;Cross-references: UNIPROT:Q9UKN7; UNIPARC:UPI0000012FABF; GB:AF144094; NID:g6224682; PII
F;1225-1887/Domain: myosin motor domain homology <MMO>

Query Match 51.6%; Score 32; DB 2; Length 3530;

Best Local Similarity 55.6%; Pred. No. 1.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRV 10
Db 3501 LCRVAVHV 3509
||||:|:|

RESULT 88
T51174
ataxia-telangiectasia mutated protein (Atm) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C:Accession: T51174; T13008
R:Garcia, V.; Salanoubat, M.; Choiane, N.; Tissier, A.F.
Nucleic Acids Res. 28, 1692-1699, 2000
A:Title: An ATM homologue from Arabidopsis thaliana: complete genomic organisation and
A:Reference number: Z25324
A:Accession: T51174
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3856 <GR>
A:Cross-references: UNIPROT:Q9M4D7; UNIPARC:UPI000009FA91; EMBL:AJ250248; PIDN:CAR86487.
A:Experimental source: cultivar Columbia
R:Choigne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, July 1999
A:Reference number: Z17586
A:Accession: T13008
A:Status: significant sequence differences
A:Molecule type: mRNA
C:Genetics:
A:Gene: atm

Query Match 51.6%; Score 32; DB 2; Length 3856;
Best Local Similarity 54.5%; Pred. No. 1.9e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVCR 12
Db 2593 LCEVPIRLCQ 2603
||||:|:|

RESULT 89
H71263
hypothetical protein TP0927 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: H71263
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: H71263
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-196 <COL>
A:Cross-references: UNIPROT:O83897; UNIPARC:UPI0000139E28; GB:AE001261; GB:AE000520; NID
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0927

Query Match 50.8%; Score 31.5; DB 2; Length 196;
Best Local Similarity 41.2%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 7; Gaps 1;

Qy 3 CRIV-----VIRVCR 12
Db 142 CSIVSQTEGDVIRICR 158
||||:|:|

RESULT 90

Ti17101
probable voltage-activated cation channel - rat
N:Alternate names: four repeat ion channel
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: Ti17101
R:Lee, J.H.; Cribbs, L.; Perez-Reyes, E.
FEBS Lett. 445, 231-236, 1999
A:Title: Cloning of a novel four repeat protein related to voltage-gated sodium and calci
A:Reference number: Z18680; MUID:99192286; PMID:10094463
A:Accession: Ti17101
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1737 <LEE>
A:Cross-references: UNIPROT:Q92165; UNIPARC:UPI00000E703E; EMBL:AF078779; NID:G3800829; I
A:Experimental source: strain Sprague-Dawley; Brain

Query Match 50.8%; Score 31.5; DB 2; Length 1737;
Best Local Similarity 58.3%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 RLCRIV-VIRVC 11
Db 43 RICAIISVISVC 54
||||:|:|

RESULT 91
D81789
hypothetical protein NMA2167 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: D81789
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: D81789
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <PAR>
A:Cross-references: UNIPROT:Q9JSS0; UNIPARC:UPI00000C4D57; GB:AL162758; GB:AL157959; NID:
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA2167

Query Match 50.0%; Score 31; DB 2; Length 62;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
Db 11 CRLKILBIC 19
||||:|:|

RESULT 92
F82564
hypothetical protein XF2373 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: F82564
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82564
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <SIM>
A:Cross-references: UNIPROT:Q9PAX2; UNIPARC:UPI00000C2A12; GB:AE004047; GB:AE003849; NID:
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF2373

Query Match 50.0%; Score 31; DB 2; Length 108;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LCRIVIVRVC 12
:|:|:|

Db 42 ICDVWVAMCCR 52

RESULT 93

BORT1

prostatic steroid-binding protein chain C1 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 09-Jul-2004

C;Accession: A93286; A93248; A90348; S42615; A03252

R;Parker, M.; Needham, M.; White, R.
Nature 298, 92-94, 1982

A;Title: Prostatic steroid binding protein: gene duplication and steroid binding.

A;Reference number: A93286; MUID:82220075; PMID:6896362

A;Accession: A93286

A;Molecule type: mRNA

A;Residues: 1-111 <PAR>

A;Cross-references: UNIPROT:P02782; UNIPARC:UPI0000174462

R;Liao, S.; Chen, C.; Huang, I.Y.
J. Biol. Chem. 257, 122-125, 1982

A;Title: Prostate alpha-protein. Complete amino acid sequence of the component that inhib

A;Reference number: A92348; MUID:82075873; PMID:7198120

A;Accession: A92348

A;Molecule type: protein

A;Residues: 24-73,'D',75-89,'E',91,'G',93-111 <LIA>

A;Cross-references: UNIPARC:UPI0000174463

R;Delaey, B.; Rombauts, W.; Volckaert, G.; Peeters, B.; Mous, J.; Heyns, W.
Biochem. Soc. Trans 10, 51, 1982

A;Title: Identification of a complementary-DNA clone containing part of the sequence inf

A;Reference number: A90348

A;Accession: A90348

A;Molecule type: mRNA

A;Residues: 13-14,'S',16,'GS',19-65

A;Cross-references: UNIPARC:UPI0000174464

R;Delaey, B.; Dirckx, L.; Peeters, B.; Volckaert, G.; Mous, J.; Heyns, W.; Rombauts, W.
Eur. J. Biochem. 133, 645-649, 1983

A;Title: The nucleotide sequence of cDNA complementary to the C(1) component of rat pro

A;Reference number: S42615; MUID:83234456; PMID:6688048

A;Accession: S42615

A;Molecule type: mRNA

A;Residues: 1-3,'IK',6-89,'E',91,'G',93-111 <DB2>

A;Cross-references: UNIPARC:UPI000000933; EMBL:V01545; NID:g57108; PIDN:CAA24787.1; PID

C;Comment: Steroid-binding protein, the principal secretory protein in rat prostatic flu

. The chains of each dimer are linked by disulfide bonds.

C;Superfamily: uteroglobin

C;Keywords: heterotetramer; prostate; steroid binding

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-111/Product: prostatic steroid-binding protein chain C1 #status experimental <MAT>

Query Match 50.0%; Score 31; DB 1; Length 111;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVIVRVC 11
||:|:|

Db 8 LCLLIHLAVC 17

RESULT 94

RSLV14

ribosomal protein L14, chloroplast - liverwort (Marchantia polymorpha) chloroplast

C;Species: chloroplast Marchantia polymorpha

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C;Accession: A02790; S01560

R;Ohyama, K.

submitted to the EMBL Data Library, October 1986

A;Reference number: A00150

A;Accession: A02790

A;Molecule type: DNA

A;Residues: 1-122 <OHY>

A;Cross-references: UNIPROT:P06381; UNIPARC:UPI00001339F0

R;Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi

Nature 322, 572-574, 1986

A;Title: Chloroplast gene organization deduced from complete sequence of liverwort March

A;Reference number: A38014

A;Contents: annotation; gene organization, sites, features

R;Fukuzawa, H.; Kohchi, T.; Sano, T.; Shirai, H.; Umesono, K.; Inokuchi, H.; Ozeki, H.; C

J. Mol. Biol. 203, 333-351, 1988

A;Title: Structure and organization of Marchantia polymorpha chloroplast genome. III. Ger

A;Reference number: S01529; MUID:89068687; PMID:3199436

A;Accession: S01560

A;Molecule type: DNA

A;Residues: 1-122 <FOK>

A;Cross-references: UNIPARC:UPI00001339F0; GB:X04465; GB:Y00686; NID:gl1640; PIDN:CAA281;

C;Genetics:

A;Gene: rpl14

A;Genome: chloroplast

C;Superfamily: ribosomal protein L14/L17/L23

C;Keywords: chloroplast; protein biosynthesis; ribosome

F;1-122/Product: ribosomal protein L14 #status predicted <MAT>

Query Match 50.0%; Score 31; DB 1; Length 122;
Best Local Similarity 36.4%; Pred. No. 1.8e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVIVRVC 12

:|:|:|

Db 57 IVRAVIVRTCK 67

RESULT 95

R5SP14

ribosomal protein L14, chloroplast - spinach chloroplast

N;Alternate names: ribosomal protein CS-L29

C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C;Accession: S01980; S20560

R;Zhou, D.X.; Quigley, F.; Massenet, O.; Mache, R.
Mol. Gen. Genet. 216, 439-445, 1989

A;Title: Cotranscription of the S10- and spc-like operons in spinach chloroplasts and ide

A;Reference number: S01976; MUID:89313684; PMID:2747623

A;Accession: S01980

A;Molecule type: DNA

A;Residues: 1-122 <ZHO>

A;Cross-references: UNIPROT:P09596; UNIPARC:UPI000016D3F1; EMBL:X13336; NID:g12307; PIDN:

A;Accession: S20560

A;Molecule type: protein

A;Residues: 1-16 <ZHO2>

A;Cross-references: UNIPARC:UPI0000173AD9

C;Genetics:

A;Gene: rpl14

A;Genome: chloroplast

C;Superfamily: ribosomal protein L14/L17/L23

C;Keywords: chloroplast; protein biosynthesis; ribosome

F;1-122/Product: ribosomal protein L14 #status experimental <MAT>

Query Match 50.0%; Score 31; DB 1; Length 122;
 Best Local Similarity 55.6%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RIVIVRVC 12
 | | | | |
 Db 59 RAVVVRTCK 67

RESULT 96
 H83005
 hypothetical protein PA5120 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: H83005
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: AB2950; MUID:20437337; PMID:10984043
 A:Accession: H83005
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-134 <STO>
 A:Cross-references: UNIPROT:Q9HU64; UNIPARC:UPI00000C5F10; GB:AE004925; GB:AE004091; NID:10984043
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA5120

Query Match 50.0%; Score 31; DB 2; Length 134;
 Best Local Similarity 44.4%; Pred. No. 2e+02;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLCRIVVIR 9
 | | | | |
 Db 126 RICRVILSR 134

RESULT 97
 C72524
 hypothetical protein APE2168 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: C72524
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: C72524
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <KAW>
 A:Cross-references: UNIPROT:Q9Y9X1; UNIPARC:UPI000005E237; DBJ:AP0000063; NID:G5105654;
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE2168
 C:Superfamily: Aeropyrum pernix hypothetical protein APE2168

Query Match 50.0%; Score 31; DB 2; Length 136;
 Best Local Similarity 55.6%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 11
 | | | | |
 Db 67 CRVEYCRVC 75

RESULT 98
 S40195
 ribosomal protein L16 - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima
 C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
 C:Accession: S40195; E72249
 R:Sanangelantoni, A.; Tiboni, O.
 submitted to the EMBL Data Library, February 1993
 A:Reference number: S37489
 A:Accession: S40195
 A:Molecule type: DNA
 A:Residues: 1-142 <SAN>
 A:Cross-references: UNIPROT:P38509; UNIPARC:UPI0000133C43; EMBL:Z21677; NID:G437921; PIDN:R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Cotton, M.S.; Phillips, C.A.; Richardson, D.; C.M.
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: E72249
 A:Molecule type: DNA
 A:Residues: 1-142 <ARN>
 A:Cross-references: UNIPARC:UPI0000133C43; GB:AE001798; GB:AE000512; NID:G4982033; PIDN:A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: rplP
 C:Superfamily: Escherichia coli ribosomal protein L16
 C:Keywords: protein biosynthesis; ribosome

Query Match 50.0%; Score 31; DB 2; Length 142;
 Best Local Similarity 50.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
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 Db 50 CRIAMLRVMK 59

RESULT 99
 T03115
 Probable fusion protein 20 - alcelaphine herpesvirus 1
 C:Species: alcelaphine herpesvirus 1
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T03115
 R:Ensser, A.; Pflanz, R.; Fleckenstein, B.
 J. Virol. 71, 6517-6525, 1997
 A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
 A:Reference number: Z14840; MUID:97404659; PMID:9261371
 A:Accession: T03115
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-250 <ENS>
 A:Cross-references: UNIPROT:O36370; UNIPARC:UPI00000F1F26; EMBL:AF005370; NID:G2337967; I C:Superfamily: varicella-zoster virus gene 35 protein

Query Match 50.0%; Score 31; DB 2; Length 250;
 Best Local Similarity 36.4%; Pred. No. 3.3e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
 | | | | |
 Db 85 RVCYVVELKTC 95

RESULT 100
 H71950
 hypothetical protein jhp0277 - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: H71950
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen
 A:Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: H71950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <ARN>
A;Cross-references: UNIPROT:Q9ZME3; UNIPARC:UPI00000D719F; GB:AE001465; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0277
C;Superfamily: Helicobacter pylori hypothetical protein jhp0277

Query Match 50.0%; Score 31; DB 2; Length 290;
Best Local Similarity 54.5%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
|| : ||| |
Db 39 RLQVAVIRDC 49

Search completed: February 15, 2006, 11:10:59
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: February 15, 2006, 11:22:16 ; Search time 18 Seconds
(without alignments)
9.474 Million cell updates/sec

Title: US-10-657-851-37

Perfect score: 62

Sequence: 1 RLCRIVIRVCR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 14211699 residues

Total number of hits satisfying chosen parameters: 107799

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	12	6	US-10-653-340-9
2	62	100.0	12	7	US-11-068-783-42
3	62	100.0	25	6	US-10-653-340-3
4	56	90.3	12	6	US-10-985-426-13
5	36	58.1	47	7	US-11-000-463-285
6	36	58.1	47	7	US-11-000-463-757
7	35	56.5	405	6	US-10-821-234-1357
8	34	54.8	131	6	US-10-467-657-8786
9	33	53.2	92	6	US-10-467-657-6350
10	33	53.2	96	6	US-10-467-657-8984
11	33	53.2	315	7	US-11-072-512-3458
12	31	50.0	136	5	US-09-978-360A-744
13	31	50.0	236	7	US-11-098-686-11423
14	31	50.0	308	6	US-10-467-657-3236
15	31	50.0	593	6	US-10-877-346-46
16	31	50.0	1495	7	US-11-019-711-111
17	30	48.4	39	6	US-10-632-150-71
18	30	48.4	39	7	US-11-073-457-71
19	30	48.4	39	7	US-11-073-460-71
20	30	48.4	57	7	US-11-234-786-577
21	30	48.4	99	6	US-10-467-657-4592
22	30	48.4	117	7	US-11-072-512-2724
23	30	48.4	178	6	US-10-508-263-46
24	30	48.4	252	6	US-10-467-657-3196
25	30	48.4	286	6	US-10-821-234-940

Sequence 42, Appl	6	US-10-632-150-42	318	48.4	30	26
Sequence 42, Appl	7	US-11-073-457-42	318	48.4	27	27
Sequence 42, Appl	7	US-11-073-460-42	318	48.4	28	28
Sequence 2, Appl	7	US-11-132-864-2	379	48.4	29	29
Sequence 6, Appl	7	US-11-132-864-6	379	48.4	30	30
Sequence 30, Appl	7	US-11-132-864-30	380	48.4	31	31
Sequence 41, Appl	7	US-11-132-864-41	388	48.4	32	32
Sequence 28, Appl	7	US-11-132-864-28	397	48.4	33	33
Sequence 48, Appl	6	US-10-632-150-48	483	48.4	34	34
Sequence 48, Appl	7	US-11-073-457-48	483	48.4	35	35
Sequence 48, Appl	7	US-11-073-460-48	483	48.4	36	36
Sequence 3148, Ap	7	US-11-072-512-3148	577	48.4	37	37
Sequence 961, App	6	US-10-821-234-961	637	48.4	38	38
Sequence 254, App	7	US-11-072-175-254	822	48.4	39	39
Sequence 8002, Ap	6	US-10-467-657-8002	112	47.6	29.5	40
Sequence 7, Appl	7	US-11-192-219-7	783	47.6	41	41
Sequence 2, Appl	7	US-11-202-330-2	894	47.6	42	42
Sequence 43, Appl	7	US-11-202-330-43	1162	47.6	43	43
Sequence 82, Appl	6	US-10-895-064-82	29	46.8	44	44
Sequence 808, App	6	US-10-485-788A-808	83	46.8	45	45
Sequence 192, App	7	US-11-053-076-192	83	46.8	46	46
Sequence 2681, Ap	7	US-11-072-512-2681	111	46.8	47	47
Sequence 1406, Ap	7	US-10-821-234-1406	113	46.8	48	48
Sequence 40, Appl	6	US-10-508-263-40	144	46.8	49	49
Sequence 2779, Ap	7	US-11-072-512-2779	159	46.8	50	50
Sequence 1878, Ap	6	US-10-467-657-1878	168	46.8	51	51
Sequence 134, App	6	US-10-793-626-134	244	46.8	52	52
Sequence 4170, Ap	6	US-10-467-657-4170	257	46.8	53	53
Sequence 1650, Ap	6	US-10-821-234-1650	331	46.8	54	54
Sequence 2, Appl	7	US-11-124-103-2	377	46.8	55	55
Sequence 54, Appl	6	US-10-632-150-54	437	46.8	56	56
Sequence 54, Appl	7	US-11-073-457-54	437	46.8	57	57
Sequence 54, Appl	7	US-11-073-460-54	437	46.8	58	58
Sequence 298, App	6	US-10-467-657-298	473	46.8	59	59
Sequence 6328, Ap	6	US-10-467-657-6328	473	46.8	60	60
Sequence 5718, Ap	6	US-10-467-657-5718	474	46.8	61	61
Sequence 7518, Ap	6	US-10-467-657-7518	474	46.8	62	62
Sequence 11247, A	7	US-11-098-686-11247	517	46.8	63	63
Sequence 31, Appl	7	US-11-147-047-31	820	46.8	64	64
Sequence 1144, Ap	6	US-10-821-234-1144	919	46.8	65	65
Sequence 75, Appl	7	US-11-037-243-75	1033	46.0	66	66
Sequence 1972, Ap	7	US-11-072-512-1972	185	46.0	67	67
Sequence 790, App	6	US-10-453-372-790	284	46.0	68	68
Sequence 776, App	6	US-10-453-372-776	290	46.0	69	69
Sequence 780, App	6	US-10-453-372-780	302	46.0	70	70
Sequence 782, App	6	US-10-453-372-782	302	46.0	71	71
Sequence 788, App	6	US-10-453-372-788	302	46.0	72	72
Sequence 792, App	6	US-10-453-372-792	302	46.0	73	73
Sequence 778, App	6	US-10-453-372-778	309	46.0	74	74
Sequence 786, App	6	US-10-453-372-786	458	46.0	75	75
Sequence 772, App	6	US-10-453-372-772	464	46.0	76	76
Sequence 774, App	6	US-10-453-372-774	464	46.0	77	77
Sequence 770, App	6	US-10-453-372-770	473	46.0	78	78
Sequence 31, Appl	6	US-10-970-847-31	13	45.2	79	79
Sequence 40, Appl	6	US-10-970-847-40	13	45.2	80	80
Sequence 72, Appl	7	US-11-214-199-72	34	45.2	81	81
Sequence 3842, Ap	6	US-10-467-657-3842	45	45.2	82	82
Sequence 3466, Ap	6	US-10-467-657-3466	45	45.2	83	83
Sequence 88, Appl	7	US-11-212-443-88	155	45.2	84	84
Sequence 86, Appl	7	US-11-212-443-86	183	45.2	85	85
Sequence 3, Appl	6	US-10-927-322-3	251	45.2	86	86
Sequence 766, App	6	US-10-453-372-766	297	45.2	87	87
Sequence 894, App	6	US-10-935-561-894	306	45.2	88	88
Sequence 2, Appl	7	US-11-044-347B-2	315	45.2	89	89
Sequence 758, App	6	US-11-157-930-2	345	45.2	90	90
Sequence 2, Appl	6	US-11-157-930-2	346	45.2	91	91
Sequence 5824, Ap	6	US-10-467-657-5824	350	45.2	92	92
Sequence 760, App	6	US-10-453-372-760	357	45.2	93	93
Sequence 3710, Ap	7	US-11-072-512-3710	358	45.2	94	94
Sequence 3087, Ap	7	US-11-072-512-3087	373	45.2	95	95
Sequence 46, Appl	7	US-11-009-658-46	395	45.2	96	96
Sequence 48, Appl	7	US-11-009-658-48	404	45.2	97	97
Sequence 8052, Ap	6	US-10-467-657-8052	425	45.2	98	98

99 28 45.2 433 7 US-11-082-389-332 Sequence 332, App
100 28 45.2 462 6 US-10-783-712A-60 Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-10-653-340-9
; Sequence 9, Application US/10653340
; Publication No. US20050250179A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Thomas K.
; APPLICANT: Jayaraman, Arul
; APPLICANT: Earthman, James C.
; TITLE OF INVENTION: Inhibition of Sulfate-Reducing-Bacteria-Mediated
; TITLE OF INVENTION: Degradation Using Bacteria Which Secrete Antimicrobials
; FILE REFERENCE: 02307E-085911US
; CURRENT APPLICATION NUMBER: US/10/653,340
; CURRENT FILING DATE: 2003-09-02
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 09/074,037
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:non-amidated
; OTHER INFORMATION: batenecin
US-10-653-340-9

Query Match 100.0%; Score 62; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
|||||

Db 1 RLCRIVVIRVCR 12
|||||

RESULT 2
US-11-068-783-42
; Sequence 42, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/11/068,783
; CURRENT FILING DATE: 2005-02-28
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-068-783-42

Query Match 100.0%; Score 62; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
|||||

Db 1 RLCRIVVIRVCR 12

RESULT 3
US-10-653-340-3
; Sequence 3, Application US/10653340
; Publication No. US20050250179A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Thomas K.
; APPLICANT: Jayaraman, Arul
; APPLICANT: Earthman, James C.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibition of Sulfate-Reducing-Bacteria-Mediated
; TITLE OF INVENTION: Degradation Using Bacteria Which Secrete Antimicrobials
; FILE REFERENCE: 02307E-085911US
; CURRENT APPLICATION NUMBER: US/10/653,340
; CURRENT FILING DATE: 2003-09-02
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 09/074,037
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pro-bactenecin
; OTHER INFORMATION: pro-region and batenecin
US-10-653-340-3

Query Match 100.0%; Score 62; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
|||||

Db 14 RLCRIVVIRVCR 25
|||||

RESULT 4
US-10-985-426-13
; Sequence 13, Application US/10985426
; Publication No. US20050250609A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: IRNA AGENTS WITH BIOCLEAVABLE TETHERS
; FILE REFERENCE: 14174-099001
; CURRENT APPLICATION NUMBER: US/10/985,426
; CURRENT FILING DATE: 2004-11-09
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary Cell Permeation Peptides
 US-10-985-426-13

Query Match 90.3%; Score 56; DB 6; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.00085;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LRCRIWIRVC 12
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 Db 1 RKCRIVIRVC 12

RESULT 5
 US-11-000-463-285
 ; Sequence 285, Application US/11000463
 ; Publication No. US20050266423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Cao, Yi-Cheng
 ; APPLICANT: Drmanac, Radjoje T.
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 785CIP4CN
 ; CURRENT APPLICATION NUMBER: US/11/000,463
 ; CURRENT FILING DATE: 2004-11-29
 ; PRIOR APPLICATION NUMBER: 10/291,265
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/922,279
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: 09/491,404
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 09/617,746
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 09/631,451
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 09/633,870
 ; PRIOR FILING DATE: 2000-09-15
 ; NUMBER OF SEQ ID NOS: 944
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 285
 ; LENGTH: 47
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-000-463-285

Query Match 58.1%; Score 36; DB 7; Length 47;
 Best Local Similarity 60.0%; Pred. No. 5.1;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVIRVC 11
 |||||
 Db 6 LCSICVRLC 15

RESULT 6
 US-11-000-463-757
 ; Sequence 757, Application US/11000463

; Publication No. US20050266423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Cao, Yi-Cheng
 ; APPLICANT: Drmanac, Radjoje T.
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 785CIP4CN
 ; CURRENT APPLICATION NUMBER: US/11/000,463
 ; CURRENT FILING DATE: 2004-11-29
 ; PRIOR APPLICATION NUMBER: 10/291,265
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/922,279
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: 09/491,404
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 09/617,746
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 09/631,451
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 09/633,870
 ; PRIOR FILING DATE: 2000-09-15
 ; NUMBER OF SEQ ID NOS: 944
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 757
 ; LENGTH: 47
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-000-463-757

Query Match 58.1%; Score 36; DB 7; Length 47;
 Best Local Similarity 60.0%; Pred. No. 5.1;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVIRVC 11
 |||||
 Db 6 LCSICVRLC 15

RESULT 7
 US-10-821-234-1357
 ; Sequence 1357, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt SEQ_genes Version 1.0
 ; SEQ ID NO 1357
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1357

Query Match 56.5%; Score 35; DB 6; Length 405;
 Best Local Similarity 63.6%; Pred. No. 44;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
||| |
Db 284 RLCRCPPVAVC 294

RESULT 8

US-10-467-657-8786
; Sequence 8786, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8786
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8786

Query Match 54.8%; Score 34; DB 6; Length 131;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 1;

Qy 1 RLCRIVVIRVC 12
|:|:|:|:|
Db 75 RICRVILL--CR 84

RESULT 9

US-10-467-657-6350
; Sequence 6350, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6350
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6350

Query Match 53.2%; Score 33; DB 6; Length 92;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 12
||| |
Db 40 RLCILVLIQIAR 51

RESULT 10

US-10-467-657-8984
; Sequence 8984, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8984
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8984

Query Match 53.2%; Score 33; DB 6; Length 96;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLCRIVVI 8
|:|:|:|
Db 75 RICRIIVI 82

RESULT 11

US-11-072-512-3458
; Sequence 3458, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3458
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3458

Query Match 53.2%; Score 33; DB 7; Length 315;

```
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVC 11
   ||| :|| :|
Db 106 RLCYLVAITEIC 116

RESULT 12
US-09-978-360A-744
; Sequence 744, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 744
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -34..-1
US-09-978-360A-744

Query Match 50.0%; Score 31; DB 5; Length 136;
Best Local Similarity 45.5%; Pred. No. 81;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVWIRVC 12
   ||| :|| :|
Db 124 LQLLMIRACR 134

RESULT 13
US-11-098-686-11423
; Sequence 11423, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
```

```
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11423
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11423

Query Match 50.0%; Score 31; DB 7; Length 236;
Best Local Similarity 36.4%; Pred. No. 1.3e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIWIRVC 11
   ||| :|| :|
Db 98 RLCVLILGLC 108

RESULT 14
US-10-467-657-3236
; Sequence 3236, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3236
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3236

Query Match 50.0%; Score 31; DB 6; Length 308;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LCRIVWIRVC 12
   ||| :|| :|
Db 233 LCRVPVARYCQ 243

RESULT 15
US-10-877-346-46
; Sequence 46, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Kekuda, Ramesh
```

```
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-877-346-46
```

```
Query Match 50.0%; Score 31; DB 6; Length 593;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY 2 LCRIVWVRC 11
|||
Db 565 LCBCVCVHVC 574
```

```
RESULT 16
US-11-019-711-111
; Sequence 111, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Sureesh G
; APPLICANT: Anderson, David W
; APPLICANT: Padiguru, Muralidhara
```

```
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 1495
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-019-711-111
```

```
Query Match 50.0%; Score 31; DB 7; Length 1495;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 IVVIRVCR 12
|||
Db 261 LVTLRVCR 268
```

```
RESULT 17
US-10-632-150-71
; Sequence 71, Application US/10632150
; Publication No. US2005025187A1
; GENERAL INFORMATION:
; APPLICANT: Chitaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-71
```

```
Query Match 48.4%; Score 30; DB 6; Length 39;
```

```
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRVIVRVC 12
Db 17 QLCRCA--RVCR 26

RESULT 18
US-11-073-457-71
; Sequence 71, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-71

Query Match 48.4%; Score 30; DB 7; Length 39;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRVIVRVC 12
Db 17 QLCRCA--RVCR 26

RESULT 19
US-11-073-460-71
; Sequence 71, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-71

Query Match 48.4%; Score 30; DB 7; Length 39;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRVIVRVC 12
Db 17 QLCRCA--RVCR 26

RESULT 20
US-11-073-460-71
```

```
US-11-234-786-577
; Sequence 577, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; TITLE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 577
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-234-786-577

Query Match 48.4%; Score 30; DB 7; Length 57;
Best Local Similarity 30.0%; Pred. No. 57;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
Db 9 QMILKRCR 18

RESULT 21
US-10-467-657-4592
; Sequence 4592, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
```

US-10-508-263-46

; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 940
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-940

Query Match 48.4%; Score 30; DB 6; Length 286;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCRIVIRV 10
|||:|:
Db 254 LCLVINRL 262

RESULT 26
US-10-632-150-42
; Sequence 42, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-42

Query Match 48.4%; Score 30; DB 6; Length 318;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRIVIRVCR 12
|||:|:
Db 159 RACRYVVL--CR 168

RESULT 27
US-11-073-457-42
; Sequence 42, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 318

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-42

Query Match 48.4%; Score 30; DB 7; Length 318;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRIVIRVCR 12
|||:|:
Db 159 RACRYVVL--CR 168

RESULT 28
US-11-073-460-42
; Sequence 42, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-42

Query Match 48.4%; Score 30; DB 7; Length 318;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRIVIRVCR 12
|||:|:
Db 159 RACRYVVL--CR 168

RESULT 29
US-11-132-864-2
; Sequence 2, Application US/11132864
; Publication No. US20050289670A1
; GENERAL INFORMATION:
; APPLICANT: Jinrui Shi
; APPLICANT: David Ertl
; APPLICANT: Lisa Hagen
; APPLICANT: Hongyu Wang
; TITLE OF INVENTION: Plant Myo-Inositol Kinase
; FILE REFERENCE: 035718/291638
; CURRENT APPLICATION NUMBER: US/11/132,864
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: 60/573,000
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Zea mays
US-11-132-864-2

Query Match 48.4%; Score 30; DB 7; Length 379;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY      1 RLCRIIVI 8
      ||||| |::
Db      172 RLCRTVLV 179

RESULT 30
US-11-132-864-6
; Sequence 6, Application US/11132864
; Publication No. US20050289670A1
; GENERAL INFORMATION:
; APPLICANT: Jinrui Shi
; APPLICANT: David Ertl
; APPLICANT: Lisa Hagen
; APPLICANT: Hongyu Wang
; TITLE OF INVENTION: Plant Myo-Inositol Kinase
; FILE REFERENCE: 035718/291638
; CURRENT APPLICATION NUMBER: US/11/132,864
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: 60/573,000
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Zea mays
; US-11-132-864-6

```

```

Query Match      48.4%; Score 30; DB 7; Length 379;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 RLCRIIVI 8
      ||||| |::
Db      172 RLCRTVLV 179

```

```

RESULT 31
US-11-132-864-30
; Sequence 30, Application US/11132864
; Publication No. US20050289670A1
; GENERAL INFORMATION:
; APPLICANT: Jinrui Shi
; APPLICANT: David Ertl
; APPLICANT: Lisa Hagen
; APPLICANT: Hongyu Wang
; TITLE OF INVENTION: Plant Myo-Inositol Kinase
; FILE REFERENCE: 035718/291638
; CURRENT APPLICATION NUMBER: US/11/132,864
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: 60/573,000
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Sorghum
; US-11-132-864-30

```

```

Query Match      48.4%; Score 30; DB 7; Length 380;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 RLCRIIVI 8
      ||||| |::
Db      173 RLCRAVLV 180

```

```

RESULT 32
US-11-132-864-41

```

```

; Sequence 41, Application US/11132864
; Publication No. US20050289670A1
; GENERAL INFORMATION:
; APPLICANT: Jinrui Shi
; APPLICANT: David Ertl
; APPLICANT: Lisa Hagen
; APPLICANT: Hongyu Wang
; TITLE OF INVENTION: Plant Myo-Inositol Kinase
; FILE REFERENCE: 035718/291638
; CURRENT APPLICATION NUMBER: US/11/132,864
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: 60/573,000
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa can be any amino acid
; US-11-132-864-41

```

```

Query Match      48.4%; Score 30; DB 7; Length 388;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 RLCRIIVI 8
      ||||| |::
Db      178 RLCRAVLV 185

```

```

RESULT 33
US-11-132-864-28
; Sequence 28, Application US/11132864
; Publication No. US20050289670A1
; GENERAL INFORMATION:
; APPLICANT: Jinrui Shi
; APPLICANT: David Ertl
; APPLICANT: Lisa Hagen
; APPLICANT: Hongyu Wang
; TITLE OF INVENTION: Plant Myo-Inositol Kinase
; FILE REFERENCE: 035718/291638
; CURRENT APPLICATION NUMBER: US/11/132,864
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: 60/573,000
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-11-132-864-28

```

```

Query Match      48.4%; Score 30; DB 7; Length 397;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 RLCRIIVI 8
      ||||| |::
Db      179 RLCRAVLV 186

```

```

RESULT 34
US-10-632-150-48
; Sequence 48, Application US/10632150

```

; Publication No. US20050251871a1
; GENERAL INFORMATION:
; APPLICANT: Chiaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS

; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-48

Query Match 48.4%; Score 30; DB 6; Length 483;
Best Local Similarity 58.3%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRIVIRVCR 12
:|||||
Db 125 QLCRCA--RVCR 134

RESULT 35

US-11-073-457-48
; Sequence 48, Application US/11073457
; Publication No. US20050260556a1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.

; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATION
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-48

Query Match 48.4%; Score 30; DB 7; Length 483;
Best Local Similarity 58.3%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRIVIRVCR 12
:|||||
Db 125 QLCRCA--RVCR 134

RESULT 36

US-11-073-460-48
; Sequence 48, Application US/11073460
; Publication No. US20050272066a1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.

; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATION

; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-48

Query Match 48.4%; Score 30; DB 7; Length 483;
Best Local Similarity 58.3%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 RLCRIVIRVCR 12
:|||||
Db 125 QLCRCA--RVCR 134

RESULT 37

US-11-072-512-3148
; Sequence 3148, Application US/11072512
; Publication No. US20060029945a1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3148
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3148

Query Match 48.4%; Score 30; DB 7; Length 577;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVCR 12
:|||||
Db 187 RLCRLLLV 194

```
RESULT 38
US-10-821-234-961
; Sequence 961, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 961
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-961

Query Match      48.4%; Score 30; DB 6; Length 637;
Best Local Similarity 75.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVVIRVCR 12
Db 38 ILSIRVCR 45

RESULT 39
US-11-072-175-254
; Sequence 254, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072.175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 254
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-175-254

Query Match      48.4%; Score 30; DB 7; Length 822;
Best Local Similarity 40.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 CRIVVIRVCR 12
Db 391 CMVTVILCR 400

RESULT 40
US-10-467-657-8002
; Sequence 8002, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
```

```
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8002
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8002

Query Match      47.6%; Score 29.5; DB 6; Length 112;
Best Local Similarity 34.8%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 RLCRIVV-----IRVCR 12
Db 28 RHCRYTVTLKPAIPAQAQIRICR 50

RESULT 41
US-11-192-219-7
; Sequence 7, Application US/11192219
; Publication No. US20050272656A1
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WSX LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/192,219
; FILING DATE: 27-Jul-2005
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,197
; FILING DATE: 20-Jun-1996
; APPLICATION NUMBER: 08/585005
; FILING DATE: 08-Jan-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0986P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-11-192-219-7

Query Match      47.6%; Score 29.5; DB 7; Length 783;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
```

```
Qy      2 LCRIVIRV-CR 12
      || : ||: ||
Db      601 LCAVVVQVRCR 612

Query Match      47.6%; Score 29.5; DB 7; Length 894;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy      2 LCRIVIRV-CR 12
      || : ||: ||
Db      601 LCAVVVQVRCR 612

RESULT 42
US-11-202-330-2
; Sequence 2, Application US/11202330
; Publication No. US20060029964A1
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/202,330
; FILING DATE: 11-AUG-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/950,149
; FILING DATE: 10-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,781
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 894 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-11-202-330-2

Qy      2 LCRIVIRV-CR 12
      || : ||: ||
Db      601 LCAVVVQVRCR 612

Query Match      47.6%; Score 29.5; DB 7; Length 894;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy      2 LCRIVIRV-CR 12
      || : ||: ||
Db      601 LCAVVVQVRCR 612

RESULT 43
US-11-202-330-43
; Sequence 43, Application US/11202330
; Publication No. US20060029964A1
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/202,330
; FILING DATE: 11-AUG-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/950,149
; FILING DATE: 10-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,781
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1162 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
```

```
; FRAGMENT TYPE: internal
US-11-202-330-43

Query Match      47.6%; Score 29.5; DB 7; Length 1162;
Best Local Similarity 50.0%; Pred. No. 8.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY      2 LCRIVIRV-CR 12
DB      601 LCAVYVQVRCR 612

RESULT 44
US-10-895-064-82
; Sequence 82, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-10-895-064-82

Query Match      46.8%; Score 29; DB 6; Length 8;
Best Local Similarity 83.3%; Pred. No. 7.7e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 VVIRVC 11
DB      1 VVIRVC 6

RESULT 45
US-10-485-788A-808
; Sequence 808, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 808
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-808
```

```
Query Match      46.8%; Score 29; DB 6; Length 83;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLCRIV 6
DB      2 RLCRLV 7

RESULT 46
US-11-053-076-192
; Sequence 192, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT APPLICATION NUMBER: US/11/053,076
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-192

Query Match      46.8%; Score 29; DB 7; Length 83;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLCRIV 6
DB      2 RLCRLV 7

RESULT 47
US-11-072-512-2681
; Sequence 2681, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUJI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
```

```

; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2681
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2681

Query Match      46.8%; Score 29; DB 7; Length 111;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CRIVWVRC 11
Db      27 CRLLPVC 35

RESULT 48
US-10-821-234-1406
; Sequence 1406, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1406
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1406

Query Match      46.8%; Score 29; DB 6; Length 113;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      2 LCRIVWVRC 11
Db      52 ICRVQVMDAC 61

RESULT 49
US-10-508-263-40
; Sequence 40, Application US/10508263
; Publication No. US20050260754A1
; GENERAL INFORMATION:
; APPLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Constructs and methods for regulating gene expression
; FILE REFERENCE: 53262-20085.00
; CURRENT APPLICATION NUMBER: US/10/508,263
; CURRENT FILING DATE: 2004-09-20
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sinapis alba
US-10-508-263-40

Query Match      46.8%; Score 29; DB 6; Length 144;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RLCRIVWVRC 11
Db      125 RVCNIRQVSV 135

RESULT 50
US-11-072-512-2779
; Sequence 2779, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2779
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2779

Query Match      46.8%; Score 29; DB 7; Length 159;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      3 CRIVWVRC 12
Db      127 CQRAIHKVCR 136

RESULT 51
US-10-467-657-1878
; Sequence 1878, Application US/10467657

```

```
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1878
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1878
```

```
Query Match 46.8%; Score 29; DB 6; Length 168;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 RIVVIRVCR 12
| : : : : |
Db 100 RHILIRTCR 108
```

```
RESULT 52
US-10-793-626-134
; Sequence 134, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-134
```

```
Query Match 46.8%; Score 29; DB 6; Length 244;
Best Local Similarity 55.6%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 LCRIVVIRV 10
| : : : : |
Db 95 LCSLLMIRV 103
```

```
RESULT 53
US-10-467-657-4170
; Sequence 4170, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

```
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4170
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4170
```

```
Query Match 46.8%; Score 29; DB 6; Length 257;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 RLCRIVV 7
| : : : : |
Db 16 RLCRLTV 22
```

```
RESULT 54
US-10-821-234-1650
; Sequence 1650, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1650
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1650
```

```
Query Match 46.8%; Score 29; DB 6; Length 331;
Best Local Similarity 22.3%; Pred. No. 3.6e+02;
Matches 2; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 4 RIVVIRVCR 12
| : : : : |
Db 205 KVIIVQACR 213
```

```
RESULT 55
US-11-124-103-2
; Sequence 2, Application US/11124103
; Publication No. US20060024699A1
; GENERAL INFORMATION:
; APPLICANT: Hitomi, Junichi
; APPLICANT: Katayama, Taiichi
; APPLICANT: Eguchi, Yutaka
; APPLICANT: Marabe, Takayuki
; APPLICANT: Tsujimoto, Yoshihide
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: A METHOD FOR EVALUATING A SUBSTANCE CAPABLE OF EFFECTING ON ENDOPI
; FILE REFERENCE: 1422-0672PUS1
; CURRENT APPLICATION NUMBER: US/11/124,103
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: JP 2004-184516
; PRIOR FILING DATE: 2004-06-23
; NUMBER OF SEQ ID NOS: 7
```


; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-103-2

Query Match 46.8%; Score 29; DB 7; Length 377;
Best Local Similarity 22.2%; Pred. No. 4e+02;
Matches 2; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RIVIRVCR 12
Db 251 KVIVQACR 259

RESULT 56
US-10-632-150-54
; Sequence 54, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/124,449
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: all Xaa positions
; OTHER INFORMATION: Xaa=unknown amino acid residue
US-10-632-150-54

Query Match 46.8%; Score 29; DB 6; Length 437;
Best Local Similarity 75.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVI 8
Db 429 RLCRCVVI 436

RESULT 57
US-11-073-457-54
; Sequence 54, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: all Xaa positions
; OTHER INFORMATION: Xaa=unknown amino acid residue
US-11-073-457-54

Query Match 46.8%; Score 29; DB 7; Length 437;
Best Local Similarity 75.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVI 8
Db 429 RLCRCVVI 436

RESULT 58
US-11-073-460-54
; Sequence 54, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: all Xaa positions
; OTHER INFORMATION: Xaa=unknown amino acid residue
US-11-073-460-54

Query Match 46.8%; Score 29; DB 7; Length 437;
Best Local Similarity 75.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVI 8
Db 429 RLCRCVVI 436

RESULT 59
US-10-467-657-298
; Sequence 298, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 298
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-298

Query Match 46.8%; Score 29; DB 6; Length 473;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 RIVVIRVC 12
|||:|:
Db 357 RIGTVRLC 365

RESULT 60
US-10-467-657-6328
; Sequence 6328, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6328
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6328

Query Match 46.8%; Score 29; DB 6; Length 473;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 RIVVIRVC 12
|||:|:
Db 357 RIGTVRLC 365

RESULT 61
US-10-467-657-5978
; Sequence 5978, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5978
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5978

Query Match 46.8%; Score 29; DB 6; Length 474;
Best Local Similarity 55.8%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RLCRIVVIR 9
|||:|:
Db 55 RLCGVKVR 63

RESULT 62
US-10-467-657-7518
; Sequence 7518, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7518
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7518

Query Match 46.8%; Score 29; DB 6; Length 474;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RLCRIVVIR 9
|||:|:
Db 55 RLCGVKVR 63

RESULT 63
US-11-098-686-11247
; Sequence 11247, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11247
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11247

Query Match 46.8%; Score 29; DB 7; Length 517;
Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LCRIVVIRVC 11
|||:|:
Db 15 LCLVWLSC 24

```
RESULT 64
US-11-147-047-31
; Sequence 31, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0016
; CURRENT APPLICATION NUMBER: US/11/147,047
; PRIOR FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-31

Query Match 46.8%; Score 29; DB 7; Length 820;
Best Local Similarity 45.5%; Pred. No. 7.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LCRIVWIRVCR 12
DB 6 LCAALLCVCR 16

RESULT 65
US-10-821-234-1144
; Sequence 1144, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1144
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1144

Query Match 46.8%; Score 29; DB 6; Length 919;
Best Local Similarity 44.4%; Pred. No. 8.4e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVWIRV 10
DB 2 LCAALLCVCR 10

RESULT 66
US-11-037-243-75
; Sequence 75, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 1033
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-75

Query Match 46.8%; Score 29; DB 7; Length 1033;
Best Local Similarity 45.5%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LCRIVWIRVCR 12
DB 552 LCKECVVERCR 562

RESULT 67
US-11-072-512-1972
; Sequence 1972, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1972
```

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; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-1972
Query Match          46.0%; Score 28.5; DB 7; Length 185;
Best Local Similarity 43.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY      2 LCRIVVIR-----VCR 12
      ||:|:|:
Db      146 LCLLVVVVAIVGWVCR 161

RESULT 68
US-10-453-372-790
; Sequence 790, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 790
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-790
Query Match          46.0%; Score 28.5; DB 6; Length 284;
Best Local Similarity 43.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY      2 LCRIVVIR-----VCR 12
      ||:|:|:
Db      245 LCLLVVVVAIVGWVCR 260

RESULT 69
US-10-453-372-776
; Sequence 776, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 790
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-790
Query Match          46.0%; Score 28.5; DB 6; Length 284;
Best Local Similarity 43.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY      2 LCRIVVIR-----VCR 12
      ||:|:|:
Db      245 LCLLVVVVAIVGWVCR 260

RESULT 70
US-10-453-372-780
; Sequence 780, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 780
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-776
Query Match          46.0%; Score 28.5; DB 6; Length 290;
Best Local Similarity 43.8%; Pred. No. 3.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY      2 LCRIVVIR-----VCR 12
      ||:|:|:
Db      248 LCLLVVVVAIVGWVCR 263
```

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; ORGANISM: Homo sapiens
US-10-453-372-780

Query Match      46.0%; Score 28.5; DB 6; Length 302;
Best Local Similarity 43.8%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy      2 LCRIVWIR-----VCR 12
      ||:|:|:
Db      263 LCLLVVVAIVAIGWVCR 278

RESULT 71
US-10-453-372-782
; Sequence 782, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 782
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-788

Query Match      46.0%; Score 28.5; DB 6; Length 302;
Best Local Similarity 43.8%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy      2 LCRIVWIR-----VCR 12
      ||:|:|:
Db      263 LCLLVVVAIVAIGWVCR 278

RESULT 72
US-10-453-372-788
; Sequence 788, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 782
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-782

Query Match      46.0%; Score 28.5; DB 6; Length 302;
Best Local Similarity 43.8%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy      2 LCRIVWIR-----VCR 12
      ||:|:|:
Db      263 LCLLVVVAIVAIGWVCR 278

RESULT 73
US-10-453-372-792
; Sequence 792, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 792
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-792
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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 788
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-788

Query Match      46.0%; Score 28.5; DB 6; Length 302;
Best Local Similarity 43.8%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy      2 LCRIVWIR-----VCR 12
      ||:|:|:
Db      263 LCLLVVVAIVAIGWVCR 278

RESULT 73
US-10-453-372-792
; Sequence 792, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 792
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-792
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```
Query Match          46.0%; Score 28.5; DB 6; Length 302;
Best Local Similarity 43.8%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY      2 LCRIVVIR-----VCR 12
      |||:|:|:|
Db      263 LCLVVVVAIGAIVGVC 278

RESULT 74
US-10-453-372-778
; Sequence 778, Application US/104533372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 778
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-786

Query Match          46.0%; Score 28.5; DB 6; Length 458;
Best Local Similarity 43.8%; Pred. No. 5.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY      2 LCRIVVIR-----VCR 12
      |||:|:|:|
Db      248 LCLVVVVAIGAIVGVC 263

RESULT 76
US-10-453-372-772
; Sequence 772, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 772
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-772

Query Match          46.0%; Score 28.5; DB 6; Length 464;
```

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Best Local Similarity 43.8%; Pred. No. 5.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy 2 LCRIVVIR-----VCR 12
Db 251 LCLLVVVAIGWVCR 266

RESULT 77
US-10-453-372-774
; Sequence 774, Application US/104533372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 774
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-774

Query Match 46.0%; Score 28.5; DB 6; Length 464;
Best Local Similarity 43.8%; Pred. No. 5.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy 2 LCRIVVIR-----VCR 12
Db 251 LCLLVVVAIGWVCR 266

RESULT 78
US-10-453-372-770
; Sequence 770, Application US/104533372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
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; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 770
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-770

Query Match 46.0%; Score 28.5; DB 6; Length 473;
Best Local Similarity 43.8%; Pred. No. 5.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

Qy 2 LCRIVVIR-----VCR 12
Db 263 LCLLVVVAIGWVCR 278

RESULT 79
US-10-970-847-31
; Sequence 31, Application US/10970847
; Publication No. US20060002854A1
; GENERAL INFORMATION:
; APPLICANT: Hanahan, Douglas
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: MOLECULES THAT SELECTIVELY HOME TO
; TITLE OF INVENTION: VASCULATURE OF PRE-MALIGNANT DYSPLASTIC LESIONS OR
; TITLE OF INVENTION: MALIGNANCIES
; FILE REFERENCE: 66821-311
; CURRENT APPLICATION NUMBER: US/10/970,847
; CURRENT FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/513,407
; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-970-847-31

Query Match 45.2%; Score 28; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CRIVVIRVCR 12
Db 1 CRVVCADGCR 10

RESULT 80
US-10-970-847-40
; Sequence 40, Application US/10970847
; Publication No. US20060002854A1
; GENERAL INFORMATION:
; APPLICANT: Hanahan, Douglas
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: MOLECULES THAT SELECTIVELY HOME TO
```

; TITLE OF INVENTION: VASCULATURE OF PRE-MALIGNANT DYSPLASTIC LESIONS OR

; TITLE OF INVENTION: MALIGNANCIES
; FILE REFERENCE: 68821-311
; CURRENT APPLICATION NUMBER: US/10/970,847
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/513,407
; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; US-10-970-847-40

Query Match 45.2%; Score 28; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 CRVIVRVC 12
||| : ||
Db 1 CRVVCADGCR 10

RESULT 81

US-11-214-199-72
; Sequence 72, Application US/11214199
; Publication No. US2006003377A1
; GENERAL INFORMATION:
; APPLICANT: HILTON, Douglas J
; APPLICANT: ALEXANDER, Warren S
; APPLICANT: VINEY, Elizabeth M
; APPLICANT: WILLSON, Tracey A
; APPLICANT: RICHARDSON, Rachael T
; APPLICANT: STARR, Robyn
; APPLICANT: NICHOLSON, Sandra E
; APPLICANT: METCALF, Donald
; APPLICANT: NICOLA, Nicos A
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC PROTEINS COMPRISING A SOCS

; FILE REFERENCE: 10976ZA
; CURRENT APPLICATION NUMBER: US/11/214,199
; CURRENT FILING DATE: 2005-08-29
; PRIOR APPLICATION NUMBER: US/09/908,805
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/302,769
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-214-199-72

Query Match 45.2%; Score 28; DB 7; Length 34;
Best Local Similarity 45.5%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LCRIVRVC 12
||| : :
Db 7 LCRFVICQYR 17

RESULT 82

US-10-467-657-3842
; Sequence 3842, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3842
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-3842

Query Match 45.2%; Score 28; DB 6; Length 45;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RLCRVIVRVC 12
||| : |||
Db 23 RLCALQRRTVCR 34

RESULT 83

US-10-467-657-3466
; Sequence 3466, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3466
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-3466

Query Match 45.2%; Score 28; DB 6; Length 49;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 CRIVRVC 11
|:::| :
Db 30 CKLIIAGC 38

RESULT 84

US-11-212-443-88
; Sequence 88, Application US/11212443
; Publication No. US20050287165A1
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/11/212,443
; CURRENT FILING DATE: 2005-08-24

; PRIOR APPLICATION NUMBER: US/09/302.626
 ; PRIOR FILING DATE: 1999-04-30
 ; PRIOR APPLICATION NUMBER: PCT/IB99/00103
 ; PRIOR FILING DATE: 1999-01-14
 ; NUMBER OF SEQ ID NOS: 195
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 88
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 US-11-212-443-88

Query Match 45.2%; Score 28; DB 7; Length 155;
 Best Local Similarity 50.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIWVIRV 10
 DB 111 RKCRVLVALMV 120

RESULT 85
 US-11-212-443-86
 ; Sequence 86, Application US/11212443
 ; Publication No. US20050287165A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Scalato, Enzo
 ; APPLICANT: Massignani, Vega
 ; APPLICANT: Rappuoli, Rino
 ; APPLICANT: Pizza, Mariagrazia
 ; APPLICANT: Grandi, Guido
 ; TITLE OF INVENTION: Meningococcal Antigens
 ; FILE REFERENCE: CHIR0159
 ; CURRENT APPLICATION NUMBER: US/11/212,443
 ; CURRENT FILING DATE: 2005-08-24
 ; PRIOR APPLICATION NUMBER: US/09/302,626
 ; PRIOR FILING DATE: 1999-04-30
 ; PRIOR APPLICATION NUMBER: PCT/IB99/00103
 ; PRIOR FILING DATE: 1999-01-14
 ; NUMBER OF SEQ ID NOS: 195
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 86
 ; LENGTH: 183
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 US-11-212-443-86

Query Match 45.2%; Score 28; DB 7; Length 183;
 Best Local Similarity 50.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIWVIRV 10
 DB 139 RKCRVLVALMV 148

RESULT 86
 US-10-927-322-3
 ; Sequence 3, Application US/10927322
 ; Publication No. US20060014158A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bittner, Michaels
 ; APPLICANT: Goppelt, Andreas
 ; TITLE OF INVENTION: Use of a Fibroblast Growth Factor-Binding Protein For The
 ; TITLE OF INVENTION: Treatment and Diagnosis of Diabetic Wound Healing Problems
 ; FILE REFERENCE: 50125/048002
 ; CURRENT APPLICATION NUMBER: US/10/927,322
 ; CURRENT FILING DATE: 2004-08-26
 ; PRIOR APPLICATION NUMBER: PCT/EP03/02122
 ; PRIOR FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: 02004299.0
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: 60/362,497

; PRIOR FILING DATE: 2002-03-06
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 3
 ; LENGTH: 251
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-927-322-3

Query Match 45.2%; Score 28; DB 6; Length 251;
 Best Local Similarity 40.0%; Pred. No. 4.2e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 2 LCR---IWIWVCR 12
 DB 132 ICRNAKSVLKRVCV 146

RESULT 87
 US-10-453-372-766
 ; Sequence 766, Application US/10453372
 ; Publication No. US2006000323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook, et al.
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
 ; FILE REFERENCE: 21402-589 A
 ; CURRENT APPLICATION NUMBER: US/10/453,372
 ; CURRENT FILING DATE: 2003-06-03
 ; PRIOR APPLICATION NUMBER: 09/789390
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: 60/185967
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 09/823187
 ; PRIOR FILING DATE: 2001-03-29
 ; PRIOR APPLICATION NUMBER: 60/195792
 ; PRIOR FILING DATE: 2000-03-10
 ; PRIOR APPLICATION NUMBER: 09/839446
 ; PRIOR FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 60/199476
 ; PRIOR FILING DATE: 2000-03-25
 ; PRIOR APPLICATION NUMBER: 09/863776
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: 60/208263
 ; PRIOR FILING DATE: 2000-05-31
 ; PRIOR APPLICATION NUMBER: 09/939398
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/227800
 ; PRIOR FILING DATE: 2000-08-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1609
 ; SOFTWARE: Curaseqlist version 0.1
 ; SEQ ID NO 766
 ; LENGTH: 297
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-453-372-766

Query Match 45.2%; Score 28; DB 6; Length 297;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVWIRV 10
 DB 167 VCAVPRV 175

RESULT 88
 US-10-995-561-894
 ; Sequence 894, Application US/10995561
 ; Publication No. US20050272054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 894
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-894

Query Match          45.2%; Score 28; DB 6; Length 306;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 1 LRCRIVIRVCR 12
Db 15 LRCRL-----LCR 22

RESULT 89
US-11-044-347B-2
; Sequence 2, Application US/11044347B
; Publication No. US20060019359A1
; GENERAL INFORMATION:
; APPLICANT: Takuji UEDA, Yuta NAKAI, Yoshiya GUNJI, Rie TAKIKAWA and Yuji JOE
; TITLE OF INVENTION: L-AMINO ACID-PRODUCING MICROORGANISM AND METHOD FOR PRODUCING L-AMINO ACID
; FILE REFERENCE: US-186
; CURRENT APPLICATION NUMBER: US/11/044,347B
; CURRENT FILING DATE: 2005-01-23
; PRIOR APPLICATION NUMBER: JP 2004-23347
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-044-347B-2

Query Match          45.2%; Score 28; DB 7; Length 315;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LRCRIVVI 8
Db 126 KLCGVVVI 133

RESULT 90
US-10-453-372-758
; Sequence 758, Application US/10453372
; Publication No. US2006003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD OF THERAPEUTIC USE
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
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; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 758
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-758

Query Match          45.2%; Score 28; DB 6; Length 345;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVVIRV 10
Db 171 VCRVVPRV 179

RESULT 91
US-11-157-930-2
; Sequence 2, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/11/157,930
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-157-930-2

Query Match          45.2%; Score 28; DB 7; Length 346;
Best Local Similarity 44.4%; Pred. No. 5.5e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LCRIVVIRV 10
Db 219 ICVLLIIRV 227

RESULT 92
US-10-467-657-5824
; Sequence 5824, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
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; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5824
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5824

Query Match 45.2%; Score 28; DB 6; Length 350;
Best Local Similarity 71.4%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCRIVV 7
:|||||
Db 290 KLCRIAV 296

RESULT 93
US-10-453-372-760
; Sequence 760, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453.372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSequist version 0.1
; SEQ ID NO 760
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-760

Query Match 45.2%; Score 28; DB 6; Length 357;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRV 10
:|||||
Db 171 VCRAVVRV 179

RESULT 94
US-11-072-512-3710
; Sequence 3710, Application US/11072512
; Publication No. US20060029945A1

; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3710
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3710

Query Match 45.2%; Score 28; DB 7; Length 358;
Best Local Similarity 36.4%; Pred. No. 5.6e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVCR 12
:|||||
Db 315 LCRSNTVLICK 325

RESULT 95
US-11-072-512-3087
; Sequence 3087, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3087
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3087

Query Match 45.2%; Score 28; DB 7; Length 373;
Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRVIV 7
|:|:|:
Db 84 RVCRLV 90

RESULT 96
US-11-009-658-46
; Sequence 46, Application US/11009658
; Publication No. US20060003430A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
; FILE REFERENCE: BB1332
; CURRENT APPLICATION NUMBER: US/11/009,658
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US/09/914,098
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/121,119
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 46
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Zea mays
US-11-009-658-46

Query Match 45.2%; Score 28; DB 7; Length 395;
Best Local Similarity 44.4%; Pred. No. 6.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRVIVRV 10
|:|:|:
Db 110 VCRVCTLRV 118

RESULT 97
US-11-009-658-48
; Sequence 48, Application US/11009658
; Publication No. US20060003430A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
; FILE REFERENCE: BB1332
; CURRENT APPLICATION NUMBER: US/11/009,658
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US/09/914,098
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/121,119
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 48
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-009-658-48

Query Match 45.2%; Score 28; DB 7; Length 404;

Best Local Similarity 44.4%; Pred. No. 6.2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRVIVRV 10
|:|:|:
Db 109 VCRVCTLRV 117

RESULT 98
US-10-467-657-8052
; Sequence 8052, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 8052
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8052

Query Match 45.2%; Score 28; DB 6; Length 425;
Best Local Similarity 55.6%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
|:|:|:
Db 234 CRVRVIASC 242

RESULT 99
US-11-082-389-332
; Sequence 332, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 332
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-332

Query Match 45.2%; Score 28; DB 7; Length 433;
Best Local Similarity 45.5%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRC 11
|:|:|:
Db 305 RVNRVLYRIC 315

RESULT 100
US-10-763-712A-60
; Sequence 60, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-763-712A-60

Query Match 45.2%; Score 28; DB 6; Length 462;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RIVVIRC 11
|:|:|:
Db 98 RVLVSVVC 105

Search completed: February 15, 2006, 11:25:18
Job time : 20 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 11:21:41 ; Search time 164 Seconds
(without alignments)
30.573 Million cell updates/sec

Title: US-10-657-851-37
Perfect score: 62
Sequence: 1 RLCRIVIRVCR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result	Query	Score	Match	Length	ID	Description	
No.							
1	62	100.0	12	3	US-09-030-619-161	Sequence 161, App	28
2	62	100.0	12	3	US-09-912-609-49	Sequence 49, Appli	29
3	62	100.0	12	3	US-09-917-340-37	Sequence 37, Appl	30
4	62	100.0	12	4	US-10-277-232-161	Sequence 161, App	31
5	62	100.0	12	4	US-10-277-233-161	Sequence 161, App	32
6	62	100.0	12	4	US-10-344-709C-4	Sequence 4, Appli	33
7	62	100.0	12	5	US-10-838-289-676	Sequence 37, Appl	34
8	62	100.0	12	5	US-10-844-837-37	Sequence 676, App	35
9	62	100.0	12	5	US-10-399-442A-5	Sequence 5, Appli	36
10	62	100.0	12	5	US-10-909-119-52	Sequence 52, Appl	37
11	62	100.0	12	5	US-10-657-851-37	Sequence 37, Appl	38
12	62	100.0	12	6	US-11-066-697-1022	Sequence 1022, Ap	39
13	62	100.0	12	6	US-11-066-697-1031	Sequence 1031, Ap	40
14	62	100.0	155	3	US-09-917-340-29	Sequence 29, Appl	41
15	62	100.0	155	4	US-10-344-709C-8	Sequence 8, Appli	42
16	62	100.0	155	5	US-10-844-837-29	Sequence 29, Appl	43
17	62	100.0	155	5	US-10-909-119-44	Sequence 44, Appl	44
18	62	100.0	155	5	US-10-657-851-29	Sequence 29, Appl	45
19	56	90.3	12	5	US-10-916-185-13	Sequence 13, Appl	46
20	56	90.3	12	5	US-10-991-286A-43	Sequence 43, Appl	47
21	56	90.3	12	5	US-10-899-912A-36	Sequence 36, Appl	48
22	56	90.3	12	6	US-11-004-379-19	Sequence 19, Appl	49
23	47.5	76.6	11	3	US-09-904-753-12	Sequence 12, Appl	50
24	44	71.0	12	4	US-10-030-619-127	Sequence 127, App	51
25	44	71.0	12	4	US-10-229-368-140	Sequence 140, App	52
26	44	71.0	12	4	US-10-225-087-118	Sequence 118, App	53
27	44	71.0	12	4	US-10-277-232-127	Sequence 127, App	54

Sequence 127, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 118, App
Sequence 42, Appli
Sequence 34320,
Sequence 356586,
Sequence 185456,
Sequence 132462,
Sequence 6, Appli
Sequence 48894, A
Sequence 14206, A
Sequence 184982,
Sequence 114215,
Sequence 14195, A
Sequence 257, App
Sequence 257, App
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Sequence 257, App
Sequence 257, App
Sequence 286841,
Sequence 349728,
Sequence 55912, A
Sequence 32, Appl
Sequence 64, Appl
Sequence 309564,
Sequence 227604,
Sequence 279410,
Sequence 18954, A
Sequence 14, Appl
Sequence 250200,
Sequence 227496,
Sequence 285, App
Sequence 757, App
Sequence 248898,
Sequence 210097,
Sequence 274478,
Sequence 343659,
Sequence 35532,
Sequence 29110, A
Sequence 27312, A
Sequence 296829,
Sequence 44488, A
Sequence 2126, Ap
Sequence 1772, Ap
Sequence 39115, A
Sequence 124578,
Sequence 22053, A
Sequence 14, Appl
Sequence 8185, Ap
Sequence 38947, A
Sequence 838, App
Sequence 10518, A
Sequence 285322,
Sequence 14197, A
Sequence 186725,
Sequence 457, App
Sequence 14200, A
Sequence 583, App
Sequence 2367, Ap
Sequence 20, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 103972,
Sequence 147668,
Sequence 212062,
Sequence 240399,
Sequence 163209,
Sequence 203122,
Sequence 33041,
Sequence 334918,
Sequence 356702,
Sequence 359307,

ALIGNMENTS

RESULT 1
US-09-030-619-161
; Sequence 161, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Efile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-030-619-161

Query Match 100.0%; Score 62; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
Db 1 RLCRIWVIRVCR 12

RESULT 2
US-09-912-609-49
; Sequence 49, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-912-609-49

Query Match 100.0%; Score 62; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
Db 1 RLCRIWVIRVCR 12

Db 1 RLCRIWVIRVCR 12
RESULT 3
US-09-917-340-37
; Sequence 37, Application US/09917340
; Patent No. US2002090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-37

Query Match 100.0%; Score 62; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
Db 1 RLCRIWVIRVCR 12

RESULT 4
US-10-277-232-161
; Sequence 161, Application US/10277232
; Publication No. US20030211537A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Efile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406C1
; CURRENT APPLICATION NUMBER: US/10/277,232
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-277-232-161

Query Match 100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
Db 1 RLCRIWVIRVCR 12

RESULT 5


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US-10-277-233-161
; Sequence 161, Application US/10277233
; Publication No. US20030232750A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 66081.406C1
; CURRENT APPLICATION NUMBER: US/10/277,233
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-277-233-161

Query Match      100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

RESULT 6
US-10-344-709C-4
; Sequence 4, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof
; FILE REFERENCE: SONN:030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-4

Query Match      100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

RESULT 7
US-10-844-837-37
; Sequence 37, Application US/10844837
; Publication No. US20050014932A1
; GENERAL INFORMATION:
; APPLICANT: Imboden, Michael

```

```

; APPLICANT: Homan, Jane
; APPLICANT: Bremel, Robert D.
; TITLE OF INVENTION: Targeted Biocides
; FILE REFERENCE: IOGEN-09014
; CURRENT APPLICATION NUMBER: US/10/844,837
; CURRENT FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-844-837-37

```

```

Query Match      100.0%; Score 62; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

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RESULT 8
US-10-838-289-676
; Sequence 676, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; FILE REFERENCE: CHRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 676
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Tumor targeting peptide
US-10-838-289-676

```

```

Query Match      100.0%; Score 62; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

```

```

RESULT 9
US-10-399-442A-5
; Sequence 5, Application US/10399442A
; Publication No. US20050063978A1
; GENERAL INFORMATION:
; APPLICANT: Jorg Fritz et al.
; TITLE OF INVENTION: Vaccine Composition Comprising an Antigen and a Peptide
; TITLE OF INVENTION: Having Adjuvant Properties
; FILE REFERENCE: SONN:031US
; CURRENT APPLICATION NUMBER: US/10/399,442A
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP01/12041
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: Austrian A 1789/00
; PRIOR FILING DATE: 2000-10-18

```

```
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-399-442A-5

Query Match      100.0%; Score 62; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLCRIWVIRVCR 12
Db      1 RLCRIWVIRVCR 12

RESULT 10
US-10-909-119-52
; Sequence 52, Application US/10909119
; Publication No. US20050079578A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; TITLE OF INVENTION: Allen-Hoffmann, Lynn
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-909-119-52

Query Match      100.0%; Score 62; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLCRIWVIRVCR 12
Db      1 RLCRIWVIRVCR 12

RESULT 11
US-10-657-851-37
; Sequence 37, Application US/10657851
; Publication No. US20050089836A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/10/657,851
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/917,340
; PRIOR FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
```

```
; ORGANISM: Bos taurus
US-10-657-851-37

Query Match      100.0%; Score 62; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLCRIWVIRVCR 12
Db      1 RLCRIWVIRVCR 12

RESULT 12
US-11-066-697-1022
; Sequence 1022, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1022
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1022

Query Match      100.0%; Score 62; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLCRIWVIRVCR 12
Db      1 RLCRIWVIRVCR 12

RESULT 13
US-11-066-697-1031
; Sequence 1031, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
```

; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1031
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-1031

Query Match 100.0%; Score 62; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

RESULT 14
US-09-917-340-29
; Sequence 29, Application US/09917340
; Patent No. US2002090369A
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; PRIOR FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-29

Query Match 100.0%; Score 62; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 144 RLCRIWVIRVCR 155

RESULT 15
US-10-344-709C-8
; Sequence 8, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof
; FILE REFERENCE: SONN-030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-8

Query Match 100.0%; Score 62; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 144 RLCRIWVIRVCR 155

RESULT 16
US-10-844-837-29
; Sequence 29, Application US/10844837
; Publication No. US20050014932A1
; GENERAL INFORMATION:
; APPLICANT: Imboden, Michael
; APPLICANT: Homan, Jane
; APPLICANT: Bremel, Robert D.
; TITLE OF INVENTION: Targeted Biocides
; FILE REFERENCE: IOGEN-09014
; CURRENT APPLICATION NUMBER: US/10/844,837
; CURRENT FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-844-837-29

Query Match 100.0%; Score 62; DB 5; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 144 RLCRIWVIRVCR 155

RESULT 17
US-10-909-119-44
; Sequence 44, Application US/10909119
; Publication No. US20050079578A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; APPLICANT: Allen-Hoffmann, Lynn
; TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-909-119-44

Query Match 100.0%; Score 62; DB 5; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |

```
Db      144 RLCRIVVIRVCR 155

RESULT 18
US-10-657-851-29
; Sequence 29, Application US/10657851
; Publication No. US2005009836A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/10/657,851
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/917,340
; PRIOR FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-657-851-29

Query Match      100.0%; Score 62; DB 5; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVCR 12
      |||||
Db      144 RLCRIVVIRVCR 155

RESULT 19
US-10-916-185-13
; Sequence 13, Application US/10916185
; Publication No. US20050107325A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kesavan, Venkatasamy
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: MODIFIED iRNA AGENTS
; FILE REFERENCE: 14174-091001
; CURRENT APPLICATION NUMBER: US/10/916,185
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 60/510,246
; PRIOR FILING DATE: 2003-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-916-185-13

Query Match      90.3%; Score 56; DB 5; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVCR 12
      |||||
Db      1 RLCRIVVIRVCR 12

RESULT 20
US-10-991-286A-43
; Sequence 43, Application US/10991286A
; Publication No. US20050186591A1
; GENERAL INFORMATION:
; APPLICANT: Bumcrot, David
; APPLICANT: Farrer, Matthew J.
; APPLICANT: Maraganore, Demetrius M.
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: METHOD OF TREATING NEURODEGENERATIVE DISEASE
; FILE REFERENCE: 17574-003001
; CURRENT APPLICATION NUMBER: US/10/991,286A
; CURRENT FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: PCT/US2004/18271
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/476,947
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptide
US-10-991-286A-43

Query Match      90.3%; Score 56; DB 5; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVCR 12
      |||||
Db      1 RLCRIVVIRVCR 12

RESULT 21
US-10-899-912A-36
; Sequence 36, Application US/10899912A
; Publication No. US20050233342A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: METHODS OF PREVENTING OFF-TARGET GENE
; TITLE OF INVENTION: SILENCING
; FILE REFERENCE: 14174-088001
; CURRENT APPLICATION NUMBER: US/10/899,912A
; CURRENT FILING DATE: 2004-07-26
; PRIOR APPLICATION NUMBER: PCT/US04/011255
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/460,783
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/462,097
; PRIOR FILING DATE: 2003-04-09
```

; PRIOR APPLICATION NUMBER: US 60/461,915
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/462,894
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-899-912A-36

Query Match 90.3%; Score 56; DB 5; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.032; Mismatches 0; Indels 1; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
| | | | | | | | | |
Db 1 RKCRIVVIRVCR 12

RESULT 22
US-11-004-379-19
; Sequence 19, Application US/11004379
; Publication No. US2005015337A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: IRNA CONJUGATES
; FILE REFERENCE: 14174-067001
; CURRENT APPLICATION NUMBER: US/11/004,379
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/US04/10586
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/460,783
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/462,894
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides

US-11-004-379-19

Query Match 90.3%; Score 56; DB 6; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.032; Mismatches 0; Indels 1; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
| | | | | | | | | |
Db 1 RKCRIVVIRVCR 12

RESULT 23
US-09-904-753-12
; Sequence 12, Application US/09904753
; Publication No. US20030092612A1
; GENERAL INFORMATION:
; APPLICANT: Lynos, Robert T
; TITLE OF INVENTION: Use of Antimicrobial Peptides as Preservatives in
; TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions,
; TITLE OF INVENTION: Emulsions, and Suspensions
; FILE REFERENCE: 2973 ver 2
; CURRENT APPLICATION NUMBER: US/09/904,753
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: WO 96/25183
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: cow
US-09-904-753-12

Query Match 76.6%; Score 47.5; DB 3; Length 11;
Best Local Similarity 91.7%; Pred. No. 0.62; Mismatches 0; Indels 1; Gaps 1;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RLCRIVVIRVCR 12
| | | | | | | | | |
Db 1 RLCCRVVIRVCR 11

RESULT 24
US-09-030-619-127
; Sequence 127, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfe, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 127
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-127

Query Match 71.0%; Score 44; DB 3; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.4; Mismatches 0; Indels 2; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

```

QY      1 RLCRIVVIRVCR 12
Db      1 RLRIVVIRVAR 12

RESULT 25
US-10-229-368-140
; Sequence 127, Application US/10229368
; Publication No. US20030148945A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Efile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIHISTAMICS
; FILE REFERENCE: 660081.406C1
; CURRENT APPLICATION NUMBER: US/10/277,232
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 127
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-10-277-232-127

Query Match      71.0%; Score 44; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 RLCRIVVIRVCR 12
Db      1 RLRIVVIRVAR 12

RESULT 28
US-10-277-233-127
; Sequence 127, Application US/10277233
; Publication No. US20030232750A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Efile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIHISTAMICS
; FILE REFERENCE: 660081.406C1
; CURRENT APPLICATION NUMBER: US/10/277,233
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 127
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-10-277-233-127

Query Match      71.0%; Score 44; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 RLCRIVVIRVCR 12
Db      1 RLRIVVIRVAR 12

RESULT 29
US-10-308-905A-3
; Sequence 3, Application US/10308905A

```

```
; Publication No. US20040001803A1
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, Robert E. W.
; APPLICANT: UNIVERSITY OF BRITISH COLUMBIA
; TITLE OF INVENTION: FORMULATIONS THEREOF
; FILE REFERENCE: 66081.417C1
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 10/865,687
; APPLICANT: FINLAY, B. Brett
; APPLICANT: GOUGH SCOTT, Monisha
; APPLICANT: BOWDISH, Dawn
; APPLICANT: ROSENBERGER, Carrie Melissa
; APPLICANT: STEVENS POWERS, Jon-Paul
; TITLE OF INVENTION: EFFECTORS OF INNATE IMMUNITY
; FILE REFERENCE: UBC1180-1
; CURRENT APPLICATION NUMBER: US/10/308,905A
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/336,632
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bovine
US-10-308-905A-3

Query Match 71.0%; Score 44; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVCR 12
Db 1 RLARIVIRVAR 12

RESULT 30
US-10-661-471-3
; Sequence 3, Application US/10661471
; Publication No. US20040180038A1
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, Robert E. W.
; APPLICANT: UNIVERSITY OF BRITISH COLUMBIA
; APPLICANT: FINLAY, B. Brett
; APPLICANT: GOUGH SCOTT, Monisha
; APPLICANT: BOWDISH, Dawn
; APPLICANT: ROSENBERGER, Carrie Melissa
; APPLICANT: STEVENS POWERS, Jon-Paul
; TITLE OF INVENTION: EFFECTORS OF INNATE IMMUNITY DETERMINATION
; FILE REFERENCE: UBC1180-2
; CURRENT APPLICATION NUMBER: US/10/661,471
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 10/308,905
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/336,632
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bovine
US-10-661-471-3

Query Match 71.0%; Score 44; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVCR 12
Db 1 RLARIVIRVAR 12

RESULT 31
US-10-865-687-118
; Sequence 118, Application US/10865687
; Publication No. US20050049182A1
; GENERAL INFORMATION:
; APPLICANT: Krieser, Timothy J.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND
; FILE REFERENCE: 66081.417C1
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 10/865,687
; PRIOR APPLICATION NUMBER: US 10/225,087
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin analog
US-10-865-687-118

Query Match 71.0%; Score 44; DB 5; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVCR 12
Db 1 RLARIVIRVAR 12

RESULT 32
US-10-338-777-42
; Sequence 42, Application US/10338777
; Publication No. US20030188343A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: United States Department of Agriculture
; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Haudenschild, Christian D.
; APPLICANT: Buckler, Edward S.
; TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants
; FILE REFERENCE: 37-000510US
; CURRENT APPLICATION NUMBER: US/10/338,777
; CURRENT FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-338-777-42

Query Match 67.7%; Score 42; DB 4; Length 662;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 12
Db 69 VCQVSVRVC 79

RESULT 33
US-10-425-115-342320
; Sequence 342320, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 342320
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(762)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_7535C.1.pep
US-10-425-115-342320

Query Match 67.7%; Score 42; DB 4; Length 762;
Best Local Similarity 33.3%; Pred. No. 2.3e+02;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
Db 262 RICSIIIVTICR 273
|:|:|:|:|:|

RESULT 34
US-10-425-115-356586
; Sequence 356586, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 356586
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_88379C.1.pep
US-10-425-115-356586

Query Match 64.5%; Score 40; DB 4; Length 51;
Best Local Similarity 41.7%; Pred. No. 38;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
Db 12 KFCRVLVQQCR 23
|:|:|:|:|

RESULT 35
US-10-425-115-185456
; Sequence 185456, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 185456
; LENGTH: 174
; TYPE: PRT

; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_100723C.1.pep
US-10-425-115-185456

Query Match 64.5%; Score 40; DB 4; Length 174;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 11
Db 150 LCRLIVLVC 159
|:|:|:|:|

RESULT 36
US-10-437-963-132462
; Sequence 132462, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 132462
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34429C.1.pep
US-10-437-963-132462

Query Match 64.5%; Score 40; DB 4; Length 560;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
Db 246 RVQVVVAVCK 257
|:|:|:|:|

RESULT 37
US-10-361-522-6
; Sequence 6, Application US/10361522
; Publication No. US20030232406A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, John B
; APPLICANT: Sloma, Alan
; APPLICANT: Pero, Janice G
; APPLICANT: Hatch, Randolph T
; APPLICANT: Hermann, Theron
; APPLICANT: Erdenberger, Thomas
; TITLE OF INVENTION: BACTERIAL STRAINS WHICH OVERPRODUCE RIBOFLAVIN
; FILE REFERENCE: 13604 US6 (C38435/129129)
; CURRENT APPLICATION NUMBER: US/10/361,522
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 09/306,615
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1778
; TYPE: PRT
; ORGANISM: Bacillus subtilis

US-10-361-522-6

Query Match 64.5%; Score 40; DB 4; Length 1778;
 Best Local Similarity 60.0%; Pred. No. 1e+03;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 11

Db 1517 LCNLVVFRIC 1526

RESULT 38

US-10-767-701-48894
 ; Sequence 48894, Application US/10767701
 ; Publication No. US20040172684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53535)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO 48894
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(125)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; OTHER INFORMATION: Clone ID: LIB3476-019-P1-K1-E12.pep
 US-10-767-701-48894

Query Match 62.9%; Score 39; DB 4; Length 125;
 Best Local Similarity 66.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11

Db 102 CRLVIRSC 110

RESULT 39

US-10-732-923-14206
 ; Sequence 14206, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 14206
 ; LENGTH: 194
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(194)
 ; OTHER INFORMATION: unsure at all Xaa locations
 US-10-732-923-14206

Query Match 62.9%; Score 39; DB 5; Length 194;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 12

Db 94 CRLVTKACR 103

RESULT 40

US-10-425-115-184982
 ; Sequence 184982, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 184982
 ; LENGTH: 264
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(264)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; OTHER INFORMATION: Clone ID: MRT4577_100295C.1.pep
 US-10-425-115-184982

Query Match 62.9%; Score 39; DB 4; Length 264;
 Best Local Similarity 60.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 12

Db 93 CRLVTKACR 102

RESULT 41

US-10-437-963-114215
 ; Sequence 114215, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 114215
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_17928C.1.pep
 US-10-437-963-114215

Query Match 62.9%; Score 39; DB 4; Length 359;
 Best Local Similarity 63.6%; Pred. No. 3.4e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LCRIVVIRVC 11

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Db      154 RLCRRVLVDVC 164
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; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-257

Query Match      61.3%; Score 38; DB 3; Length 50;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      3 CRIVVIRVC 12
||||| |::||
Db      375 CRIVVTKSCR 384

RESULT 43
US-09-974-879-257
; Sequence 257, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-401-257

Query Match      61.3%; Score 38; DB 4; Length 50;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
|:|:|:|:|
Db      28 VCQYVIVRVC 37
|:|:|:|:|

RESULT 44
US-10-621-401-257
; Sequence 257, Application US/10621401
; Publication No. US20040038277A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2C1
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/974,879
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-401-257

Query Match      61.3%; Score 38; DB 4; Length 50;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
|:|:|:|:|
Db      28 VCQYVIVRVC 37
|:|:|:|:|

RESULT 45
US-09-305-736-257
; Sequence 257, Application US/09305736
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Db      154 RLCRRVLVDVC 164
||||| |::||
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-257

Query Match      61.3%; Score 38; DB 3; Length 50;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
|:|:|:|:|
Db      28 VCQYVIVRVC 37
|:|:~|:~|:~|

RESULT 44
US-10-621-401-257
; Sequence 257, Application US/10621401
; Publication No. US20040038277A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2C1
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 09/974,879
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-401-257

Query Match      61.3%; Score 38; DB 4; Length 50;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
|:|:~|:~|:~|
Db      28 VCQYVIVRVC 37
|:~|:~|:~|

RESULT 45
US-09-305-736-257
; Sequence 257, Application US/09305736
```

```
; Publication No. US20030088078A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/305,736
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
; EARLIER FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/064,911
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,988
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,987
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,908
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,984
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,985
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/066,094
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,100
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals stop translation
US-09-305-736-257
```

```
Query Match 61.3%; Score 38; DB 3; Length 51;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 LCRIVVIRVC 11
:|: |:|:|
Db 28 VCQYVIVRVC 37
```

```
RESULT 46
US-09-818-683-257
; Sequence 257, Application US/09818683
; Publication No. US20030211472A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/818,683
; CURRENT FILING DATE: 2001-03-28
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 51
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals stop translation
US-09-818-683-257
Query Match 61.3%; Score 38; DB 3; Length 51;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LCRIVVIRVC 11
:|: |:|:|
Db 28 VCQYVIVRVC 37
RESULT 47
US-09-818-683-257
; Sequence 257, Application US/09818683
; Publication No. US20040185440A9
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/818,683
; CURRENT FILING DATE: 2001-03-28
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals stop translation
US-09-818-683-257
```

```
Query Match 61.3%; Score 38; DB 3; Length 51;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 2 LCRIVVIRVC 11
:|: |:|:|
Db 28 VCQYVIVRVC 37
```

```
RESULT 48
US-10-425-115-286841
; Sequence 286841, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286841
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_24694C.1.pep
US-10-425-115-286841
```

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Query Match 61.3%; Score 38; DB 4; Length 72;
```

```
; Sequence 32, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-041-018-32

Query Match      61.3%; Score 38; DB 4; Length 343;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
      ||::||::||
Db      2 LCKIIIMRPC 11

RESULT 52
US-10-041-018-64
; Sequence 64, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-041-018-64

Query Match      61.3%; Score 38; DB 4; Length 343;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
      ||::||::||
Db      2 LCKIIIMRPC 11

RESULT 53
US-10-425-115-309564
; Sequence 309564, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326

; US-10-041-018-32

Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
      ||::||::||
Db      20 LCACVLRIC 29

RESULT 49
US-10-425-115-349728
; Sequence 349728, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 349728
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_82126C.1.pep
; US-10-425-115-349728

Query Match      61.3%; Score 38; DB 4; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LCRIVVIRV 10
      ||::||::||
Db      21 LCRVLVVRV 29

RESULT 50
US-10-767-701-55912
; Sequence 55912, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 55912
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30934332.pep
; US-10-767-701-55912

Query Match      61.3%; Score 38; DB 4; Length 156;
Best Local Similarity 45.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 12
      ||::||::||
Db      96 ICRLLSLRIC 106

RESULT 51
; US-10-041-018-32
```

```
; Sequence 32, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-041-018-32

Query Match      61.3%; Score 38; DB 4; Length 343;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
      ||::||::||
Db      2 LCKIIIMRPC 11

RESULT 52
US-10-041-018-64
; Sequence 64, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-041-018-64

Query Match      61.3%; Score 38; DB 4; Length 343;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
      ||::||::||
Db      2 LCKIIIMRPC 11

RESULT 53
US-10-425-115-309564
; Sequence 309564, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
```

; SEQ ID NO 309564
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_45385C.1.pep
US-10-425-115-309564

Query Match 59.7%; Score 37; DB 4; Length 72;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVRVC 11
||| |
Db 31 QLCGAVRVC 41
||| |

RESULT 54
US-10-425-115-227604
; Sequence 227604, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 227604
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139170C.1.pep
US-10-425-115-227604

Query Match 59.7%; Score 37; DB 4; Length 105;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVRVC 11
||| |
Db 54 LCLRVVPPC 63
||| |

RESULT 55
US-10-425-115-279410
; Sequence 279410, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 279410
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_186401C.1.pep
US-10-425-115-279410

Query Match 59.7%; Score 37; DB 4; Length 121;

Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RLCRIVRVC 11
||| |
Db 108 RLCCIAAVRLC 118
||| |

RESULT 56
US-11-097-143-18954
; Sequence 18954, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18954
; LENGTH: 378
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-18954

Query Match 59.7%; Score 37; DB 6; Length 378;
Best Local Similarity 58.3%; Pred. No. 7.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVRVC 12
||| |
Db 49 REARVFLRVC 60
||| |

RESULT 57
US-10-132-134-14
; Sequence 14, Application US/10132134
; Publication No. US20030171562A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
; FILE REFERENCE: 3012-2US
; CURRENT APPLICATION NUMBER: US/10/132,134
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1953
; TYPE: PRT
; ORGANISM: Streptomyces platensis subsp. roseaceus

US-10-132-134-14

Query Match 59.7%; Score 37; DB 4; Length 1953;
Best Local Similarity 54.5%; Pred. No. 3.3e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVC 11
| | | : | | : | |
Db 51 RVCVVVVKVC 61

RESULT 58

US-10-425-115-250200
; Sequence 250200, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 250200
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_159770C.1.pep
US-10-425-115-250200

Query Match 58.9%; Score 36.5; DB 4; Length 98;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 1 RLCRIVV-IRVCR 12
| | | | : | : | |
Db 39 RLCRLLVFFEICR 51

RESULT 59

US-10-425-115-227496
; Sequence 227496, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 227496
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(168)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139072C.1.pep
US-10-425-115-227496

Query Match 58.9%; Score 36.5; DB 4; Length 168;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 RLCRIVVIRVCR 12
| | | : | | : | |
Db 147 RLCFVVVLR-CR 157

RESULT 60

US-10-291-265-285
; Sequence 285, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 285
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-285

Query Match 58.1%; Score 36; DB 4; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 11
| | | : | | : | |
Db 6 LCSICVLRLC 15

RESULT 61

US-10-291-265-757
; Sequence 757, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 757
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-757

Query Match 58.1%; Score 36; DB 4; Length 47;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVWVRC 11
||| :|||
Db 6 LCSICVRLC 15

RESULT 62

US-10-425-115-248898
; Sequence 248898, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 248898
; SEQ ID NO 248898
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_158583C.1.pep
US-10-425-115-248898

Query Match 58.1%; Score 36; DB 4; Length 48;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LCRIVWVRC 12
||| :|||
Db 19 RICQCIDRVC 30

RESULT 63

US-10-424-599-210097
; Sequence 210097, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 210097
; SEQ ID NO 210097
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31746C.1.pep
US-10-424-599-210097

Query Match 58.1%; Score 36; DB 4; Length 52;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LCRIVWVRC 10
||| :|||
Db 18 ICRIIIIVK 26

RESULT 64

US-10-424-599-274478
; Sequence 274478, Application US/10424599
; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274478
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89876C.1.pep
US-10-424-599-274478

Query Match 58.1%; Score 36; DB 4; Length 52;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVWVRC 11
||| :|||
Db 18 MCQVITTC 27

RESULT 65

US-10-425-115-343659
; Sequence 343659, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 343659
; SEQ ID NO 343659
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76579C.1.pep
US-10-425-115-343659

Query Match 58.1%; Score 36; DB 4; Length 54;
Best Local Similarity 70.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LCRIVWVRC 10
||| :|||
Db 19 RLCRAVVVV 28

RESULT 66

US-10-425-115-355532
; Sequence 355532, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115

```
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 35532
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87410C.1.pep
US-10-425-115-35532

Query Match      58.1%; Score 36; DB 4; Length 55;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LCRIVVIRVC 11
   |||||: ||
Db 43 LRCRLSSRSC 53

RESULT 67
US-10-029-386-29110
; Sequence 29110, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29110
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR11.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.88
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: P39766, EVALUATION 7.10e+00
US-10-029-386-29110

Query Match      58.1%; Score 36; DB 4; Length 75;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVC 11
   |||||: ||
Db 19 LCRLLWLHVC 28

RESULT 68
US-11-097-143-27312
; Sequence 27312, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
;

; CURRENT FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27312
; LENGTH: 75
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-27312

Query Match      58.1%; Score 36; DB 6; Length 75;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIRVCR 12
   ||: |||
Db 45 CRVCKLRVCK 54

RESULT 69
US-10-425-115-296829
; Sequence 296829, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 296829
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_33782C.1.pep
US-10-425-115-296829

Query Match      58.1%; Score 36; DB 4; Length 113;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 12
   ||||: |||
Db 81 LCRFPFLRACR 91

RESULT 70
US-10-450-763-44488
; Sequence 44488, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
```


; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44488
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(115)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-44488

Query Match 58.1%; Score 36; DB 5; Length 115;
Best Local Similarity 58.3%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIVIRVC 12
| | | | |
DB 101 RRCRLAHRPCR 112

RESULT 71

US-10-017-161-2126
; Sequence 2126, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2126
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-2126

Query Match 58.1%; Score 36; DB 4; Length 269;
Best Local Similarity 54.5%; Pred. No. 7.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIVIRVC 11
| | | | |
DB 91 RVCVFIVIRVC 101

RESULT 72

US-10-292-798-1772
; Sequence 1772, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161

; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1772
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-1772

Query Match 58.1%; Score 36; DB 4; Length 269;
Best Local Similarity 54.5%; Pred. No. 7.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIVIRVC 11
| | | | |
DB 91 RVCVFIVIRVC 101

RESULT 73

US-10-425-114-39115
; Sequence 39115, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39115
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701179351_FLI.pep
US-10-425-114-39115

Query Match 58.1%; Score 36; DB 4; Length 284;
Best Local Similarity 54.5%; Pred. No. 7.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLCRIVIRVC 11
| | | | |
DB 187 RACRVNPLRVC 197

RESULT 74

US-10-437-963-124578
; Sequence 124578, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

```
; SEQ ID NO 124578
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27302C.1.pep
US-10-437-963-124578

Query Match      58.1%; Score 36; DB 4; Length 364;
Best Local Similarity 54.5%; Pred. No. 1e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 RLCRIVVIRVC 11
Db      162 RLCRRVLVLC 172

RESULT 75
US-10-369-493-22053
; Sequence 22053, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22053
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22053

Query Match      58.1%; Score 36; DB 4; Length 391;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      2 LCRIVVIRVC 11
Db      327 LCRIVLVKIC 336

RESULT 76
US-10-355-430-14
; Sequence 14, Application US/10355430
; Publication No. US20030108332A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Jinzhao
; TITLE OF INVENTION: Amino Acid Transporters
; FILE REFERENCE: REN-00-121
; CURRENT APPLICATION NUMBER: US/10/355,430
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Zea mays
US-10-355-430-14

Query Match      58.1%; Score 36; DB 4; Length 462;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RLCRIVVIRVC 11

; SEQ ID NO 124578
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27302C.1.pep
US-10-437-963-124578

Query Match      58.1%; Score 36; DB 4; Length 364;
Best Local Similarity 54.5%; Pred. No. 1e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 RLCRIVVIRVC 11
Db      162 RLCRRVLVLC 172

RESULT 77
US-10-739-930-8185
; Sequence 8185, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 8185
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(471)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C419_4.p
US-10-739-930-8185

Query Match      58.1%; Score 36; DB 5; Length 471;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RLCRIVVIRVC 11
Db      372 RACRVNPLRVC 382

RESULT 78
US-10-425-114-38947
; Sequence 38947, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38947
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701142782_FLI.pep
US-10-425-114-38947

Query Match      58.1%; Score 36; DB 4; Length 517;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 CRIVVIRVC 12
Db      232 CRVVVKSCR 241

RESULT 79
US-10-389-566-838
```

```
; Sequence 838, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 838
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (164)..(164)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (177)..(177)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (520)..(520)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (537)..(537)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; US-10-389-566-838

Query Match      58.1%; Score 36; DB 4; Length 537;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
Matches      6; Conservative      2; Mismatches      3; Indels      0; Gaps      0;

Qy      2 LCRIVWIRVCR 12
Db      277 MCRVSWTRVCR 287

RESULT 80
US-10-739-930-10518
; Sequence 10518, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
```

```
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 10518
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(645)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C460_1.p
; US-10-739-930-10518

Query Match      58.1%; Score 36; DB 5; Length 645;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches      6; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

Qy      2 LCRIVWIRVCR 11
Db      182 ICRCWINAC 191

RESULT 81
US-10-424-599-285322
; Sequence 285322, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 285322
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(682)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99675C.1.pep
; US-10-424-599-285322

Query Match      58.1%; Score 36; DB 4; Length 682;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches      6; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

Qy      3 CRIVWIRVCR 12
Db      269 CRVVKKSCR 278

RESULT 82
US-10-732-923-14197
; Sequence 14197, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
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; SEQ ID NO 14197
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(695)
; OTHER INFORMATION: unsure at all xaa locations
US-10-732-923-14197

Query Match      58.1%; Score 36; DB 5; Length 695;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CRVWIRVCR 12
Db      270 CRVWVKSCR 279

RESULT 83
US-10-437-963-186725
; Sequence 186725, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 186725
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_83498C.1.pep
US-10-437-963-186725

Query Match      58.1%; Score 36; DB 4; Length 698;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CRVWIRVCR 12
Db      387 CRLVITKSCR 396

RESULT 84
US-10-732-923-457
; Sequence 457, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 457
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-732-923-457
```

```
Query Match      58.1%; Score 36; DB 5; Length 708;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CRVWIRVCR 12
Db      387 CRLVITKSCR 396
```

```
RESULT 85
US-10-732-923-14200
; Sequence 14200, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 14200
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-10-732-923-14200
```

```
Query Match      58.1%; Score 36; DB 5; Length 708;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CRVWIRVCR 12
Db      387 CRLVITKSCR 396
```

```
RESULT 86
US-10-310-154-583
; Sequence 583, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhuo
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A.
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
```

; APPLICANT: McKiel, Christine L.
 ; APPLICANT: Miller, Philip W.
 ; APPLICANT: Padmavathi, Manchikanti
 ; APPLICANT: Parnell, Laurence D.
 ; APPLICANT: Start, William G.
 ; APPLICANT: Tennesen, Dan
 ; APPLICANT: Vidya, K.R.
 ; APPLICANT: Wang, Haiyun
 ; APPLICANT: Xin, Zhanguo
 ; APPLICANT: Xu, Nanfei
 ; APPLICANT: Yang, Chunzhi
 ; APPLICANT: Zeng, Xiaoping
 ; APPLICANT: Zhang, Qiang
 ; APPLICANT: Zhao, Yajuan
 ; APPLICANT: Zhou, Li
 ; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
 ; FILE REFERENCE: 38-15(52796)B
 ; CURRENT APPLICATION NUMBER: US/10/310,154
 ; CURRENT FILING DATE: 2002-12-04
 ; PRIOR APPLICATION NUMBER: 60/337,358
 ; PRIOR FILING DATE: 2001-12-04
 ; NUMBER OF SEQ ID NOS: 736
 ; SEQ ID NO 583
 ; LENGTH: 709
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-10-310-154-593

Query Match 58.1%; Score 36; DB 4; Length 709;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
 |||: : ||
 Db 387 CRLVITKSCR 396

RESULT 87
 ; Sequence 2367, Application US/11097143
 ; Publication No. US20050208558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; APPLICANT: et al.
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 ; TITLE OF INVENTION: DROSOPHILA GENES.
 ; FILE REFERENCE: CL000728
 ; CURRENT APPLICATION NUMBER: US/11/097,143
 ; CURRENT FILING DATE: 2005-04-04
 ; PRIOR APPLICATION NUMBER: 60/157,832
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/160,191
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 60/161,932
 ; PRIOR FILING DATE: 1999-10-28
 ; PRIOR APPLICATION NUMBER: 60/164,769
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/173,383
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/175,693
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 60/184,831
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/191,637
 ; PRIOR FILING DATE: 2000-03-23
 ; NUMBER OF SEQ ID NOS: 43008
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2367
 ; LENGTH: 762
 ; TYPE: PRT
 ; ORGANISM: DROSOPHILA
 US-11-097-143-2367

Query Match 58.1%; Score 36; DB 6; Length 762;
 Best Local Similarity 45.5%; Pred. No. 2e+03;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVIVRVC 11
 |||: : ||
 Db 28 RVCRVFRQVC 38

RESULT 88
 ; US-10-441-926-20
 ; Sequence 20, Application US/10441926
 ; Publication No. US20040115621A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodrigo, Allen
 ; APPLICANT: Ross, Howard A.
 ; APPLICANT: Mullins, James I.
 ; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
 ; FILE REFERENCE: 08987-011001
 ; CURRENT APPLICATION NUMBER: US/10/441,926
 ; CURRENT FILING DATE: 2003-05-19
 ; PRIOR APPLICATION NUMBER: PCT/US01/05288
 ; PRIOR FILING DATE: 2001-02-18
 ; PRIOR APPLICATION NUMBER: US 60/183,659
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 861
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificially generated peptide
 US-10-441-926-20

Query Match 58.1%; Score 36; DB 4; Length 861;
 Best Local Similarity 54.5%; Pred. No. 2.2e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVIVRVC 11
 |||: : ||
 Db 147 RNCRLTIAIC 157

RESULT 89
 ; US-10-441-926-22
 ; Sequence 22, Application US/10441926
 ; Publication No. US20040115621A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodrigo, Allen
 ; APPLICANT: Ross, Howard A.
 ; APPLICANT: Mullins, James I.
 ; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
 ; FILE REFERENCE: 08987-011001
 ; CURRENT APPLICATION NUMBER: US/10/441,926
 ; CURRENT FILING DATE: 2003-05-19
 ; PRIOR APPLICATION NUMBER: PCT/US01/05288
 ; PRIOR FILING DATE: 2001-02-18
 ; PRIOR APPLICATION NUMBER: US 60/183,659
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 861
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificially generated peptide
 US-10-441-926-22

Query Match 58.1%; Score 36; DB 4; Length 861;
 Best Local Similarity 54.5%; Pred. No. 2.2e+03;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRVIVRVC 11
| | | | | | | |
Db 147 RNCRLITIAIC 157

RESULT 90

US-10-441-926-24
; Sequence 24, Application US/10441926
; Publication No. US20040115621A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-011001
; CURRENT APPLICATION NUMBER: US/10/441,926
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-18
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 861
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated peptide

US-10-441-926-24

Query Match 58.1%; Score 36; DB 4; Length 861;
Best Local Similarity 54.5%; Pred. No. 2.2e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRVIVRVC 11
| | | | | | | |
Db 147 RNCRLITIAIC 157

RESULT 91

US-10-437-963-103972
; Sequence 103972, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 103972
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_101350C.1.pap

US-10-437-963-103972

Query Match 56.5%; Score 35; DB 4; Length 42;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVVIRVCR 12
| | | | | | | |
Db 29 CDLVIRLCK 38

RESULT 92

US-10-437-963-147668
; Sequence 147668, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147668
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48175C.1.pap

US-10-437-963-147668

Query Match 56.5%; Score 35; DB 4; Length 45;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRVIVRVC 10
| | | | | | | |
Db 11 RLCRVVPHV 20

RESULT 93

US-10-425-115-212062
; Sequence 212062, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 212062
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_125002C.1.pap

US-10-425-115-212062

Query Match 56.5%; Score 35; DB 4; Length 45;
Best Local Similarity 63.6%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRVIVRVC 12
| | | | | | | |
Db 33 LCRVIVRVC 43

RESULT 94
US-10-424-599-240399
; Sequence 240399, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240399
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59107C.1.pep
US-10-424-599-240399

Query Match 56.5%; Score 35; DB 4; Length 51;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
| : : : : |
Db 18 CIVVIRLC 26

RESULT 95
US-10-437-963-163209
; Sequence 163209, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163209
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62227C.1.pep
US-10-437-963-163209

Query Match 56.5%; Score 35; DB 4; Length 51;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRVIRVC 11
| : : : : |
Db 40 RTCKLSVIRSC 50

RESULT 96
US-10-425-115-203122
; Sequence 203122, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 203122
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(59)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116835C.1.pep
US-10-425-115-203122

Query Match 56.5%; Score 35; DB 4; Length 59;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLCRVIVIR 9
| : : : : |
Db 49 RLCRLIKIR 57

RESULT 97
US-10-425-115-302041
; Sequence 302041, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 302041
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_38536C.1.pep
US-10-425-115-302041

Query Match 56.5%; Score 35; DB 4; Length 74;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVCR 12
| : : : : |
Db 39 LCRILIIILIR 49

RESULT 98
US-10-425-115-334918
; Sequence 334918, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 334918
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_6855C.1.pbp
US-10-425-115-334918

Query Match          56.5%; Score 35; DB 4; Length 84;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RLCRIVVIR 9
Db      46 RFCRIVLLR 54

RESULT 99
US-10-425-115-356702
; Sequence 356702, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 356702
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(87)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_88483C.1.pbp
US-10-425-115-356702

Query Match          56.5%; Score 35; DB 4; Length 87;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 LCRIVVIRVC 11
Db      70 VCGLTIRVC 79

RESULT 100
US-10-425-115-359307
; Sequence 359307, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; ;
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; SEQ ID NO 359307
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_90856C.1.pbp
US-10-425-115-359307

Query Match          56.5%; Score 35; DB 4; Length 88;
Best Local Similarity 54.5%; Pred. No. 3.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVC 11
Db      41 QLCRGFLLRVC 51

Search completed: February 15, 2006, 11:24:55
Job time : 166 secs
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OM protein - protein search, using sw model

Run on: February 15, 2006, 11:10:31 ; Search time 47 Seconds
(without alignments)
21.109 Million cell updates/sec

Title: US-10-657-851-37

Perfect score: 62

Sequence: 1 RLCRIVIRVCR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/FCRUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	12	2	US-09-082-420-1
2	62	100.0	12	2	US-09-082-420-17
3	62	100.0	12	2	US-09-030-619-161
4	62	100.0	12	2	US-09-282-277-9
5	62	100.0	12	2	US-09-917-340-37
6	62	100.0	12	2	US-09-623-548A-1022
7	62	100.0	12	2	US-09-623-548A-1031
8	62	100.0	12	2	US-09-657-276-1022
9	62	100.0	12	2	US-09-657-276-1031
10	62	100.0	12	2	US-09-444-281-42
11	62	100.0	14	2	US-09-082-420-11
12	62	100.0	18	2	US-09-082-420-18
13	62	100.0	25	2	US-09-282-277-3
14	62	100.0	155	2	US-09-917-340-29
15	52	83.9	12	2	US-09-082-420-3
16	51.5	83.1	13	2	US-09-082-420-12
17	51.5	83.1	13	2	US-09-082-420-13
18	51.5	83.1	15	2	US-09-082-420-14
19	49	79.0	12	2	US-09-082-420-5
20	49	79.0	12	2	US-09-082-420-20
21	49	79.0	14	2	US-09-082-420-9
22	47.5	76.6	11	2	US-09-904-753-12
23	45	72.6	12	2	US-09-082-420-6
24	44	71.0	12	2	US-09-082-420-2
25	44	71.0	12	2	US-09-030-619-127
26	44	71.0	12	2	US-10-225-087-118
27	43	69.4	12	2	US-09-082-420-8
28	42	67.7	12	2	US-09-082-420-4
29	42	67.7	12	2	US-09-082-420-19
30	41	66.1	12	2	US-09-082-420-7
31	40.5	65.3	14	2	US-09-082-420-10
32	38.5	62.1	13	2	US-09-082-420-15
33	37	59.7	181	2	US-09-252-991A-30203
34	36	58.1	152	2	US-09-270-767-41347
35	36	58.1	152	2	US-09-270-767-56563
36	36	58.1	318	2	US-09-270-767-45575
37	36	58.1	334	2	US-09-107-532A-4947
38	35	56.5	228	2	US-08-911-423-6
39	35	56.5	232	2	US-08-911-423-7
40	35	56.5	234	2	US-09-512-363-2
41	35	56.5	234	2	US-09-176-200-2
42	35	56.5	234	2	US-09-915-593-2
43	35	56.5	240	2	US-09-512-363-6
44	35	56.5	240	2	US-09-176-200-6
45	35	56.5	240	2	US-09-915-593-6
46	35	56.5	241	2	US-08-911-423-4
47	35	56.5	241	2	US-09-512-363-28
48	35	56.5	241	2	US-09-915-593-28
49	35	56.5	241	2	US-08-949-016-7232
50	35	56.5	311	2	US-08-911-423-8
51	34	54.8	116	2	US-09-134-000C-6570
52	34	54.8	209	2	US-09-583-110-3039
53	34	54.8	217	2	US-09-107-433-4632
54	34	54.8	971	2	US-09-248-796A-19531
55	33	53.2	38	2	US-09-270-767-60996
56	33	53.2	69	2	US-09-270-767-50217
57	33	53.2	69	2	US-09-270-767-35000
58	33	53.2	114	2	US-09-134-000C-5671
59	33	53.2	120	2	US-09-270-767-37838
60	33	53.2	120	2	US-09-270-767-53055
61	33	53.2	166	2	US-09-270-767-45487
62	33	53.2	231	2	US-09-252-991A-26289
63	33	53.2	264	2	US-09-902-540-10473
64	33	53.2	279	2	US-09-198-452A-1201
65	33	53.2	281	2	US-09-438-185A-519
66	33	53.2	315	2	US-10-104-047-3458
67	33	53.2	396	2	US-09-809-665A-115
68	33	53.2	398	2	US-09-809-665A-50
69	33	53.2	477	1	US-07-969-267B-3
70	33	53.2	477	2	US-09-168-510-3
71	33	53.2	477	2	US-10-277-078-3
72	33	53.2	609	2	US-09-949-016-6846
73	32.5	52.4	425	2	US-09-230-371A-30
74	32.5	52.4	631	2	US-09-270-767-44123
75	32	51.6	97	2	US-09-198-452A-1019
76	32	51.6	122	2	US-09-732-210-389
77	32	51.6	126	2	US-09-902-540-16503
78	32	51.6	186	2	US-09-270-767-50263
79	32	51.6	186	2	US-09-270-767-50263
80	32	51.6	193	2	US-09-605-703B-2376
81	32	51.6	216	2	US-09-270-767-56833
82	32	51.6	257	2	US-09-270-767-33011
83	32	51.6	257	2	US-09-270-767-48228
84	32	51.6	267	2	US-09-270-767-35184
85	32	51.6	267	2	US-09-270-767-50401
86	32	51.6	308	2	US-09-540-236-2293
87	32	51.6	401	2	US-09-252-991A-26909
88	32	51.6	548	2	US-09-252-991A-20793
89	32	51.6	569	2	US-09-437-568A-12
90	32	51.6	569	2	US-09-999-248A-13
91	32	51.6	570	2	US-09-437-568A-38
92	32	51.6	570	2	US-09-437-568A-38
93	32	51.6	570	2	US-10-418-036-2
94	32	51.6	710	2	US-09-252-991A-25700
95	32	51.6	1009	2	US-09-633-146-4
96	31.5	50.8	14	2	US-09-082-420-16
97	31.5	50.8	56	2	US-09-513-999C-4573
98	31.5	50.8	57	2	US-09-471-276-1013
99	31	50.0	16	1	US-08-685-589A-141
100	31	50.0	52	2	US-09-621-976-5254

Sequence 4, Appli
Sequence 19, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 15, Appli
Sequence 30203, A
Sequence 41347, A
Sequence 56563, A
Sequence 45575, A
Sequence 4947, Ap
Sequence 6, Appli
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Sequence 28, Appli
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Sequence 519, App
Sequence 3458, Ap
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Sequence 4123, A
Sequence 1019, Ap
Sequence 389, App
Sequence 16503, A
Sequence 35046, A
Sequence 50263, A
Sequence 2376, Ap
Sequence 56833, A
Sequence 33011, A
Sequence 48228, A
Sequence 35184, A
Sequence 50401, A
Sequence 2293, Ap
Sequence 26909, A
Sequence 20793, A
Sequence 12, Appli
Sequence 13, Appli
Sequence 37, Appli
Sequence 38, Appli
Sequence 2, Appli
Sequence 25700, A
Sequence 4, Appli
Sequence 16, Appli
Sequence 4573, Ap
Sequence 1013, Ap
Sequence 141, App
Sequence 5254, Ap

ALIGNMENTS

RESULT 1
US-09-082-420-1 Application US/09082420

; Sequence 17, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-1

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
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Db 1 RLCRIWVIRVCR 12

RESULT 2
US-09-082-420-17

; Sequence 17, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: amidated Arg at C-terminus
US-09-082-420-17

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

RESULT 3
US-09-030-619-161

; Sequence 161, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfe, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 66081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-030-619-161

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

RESULT 4

US-09-282-277-9
; Sequence 9, Application US/09282277
; Patent No. 6630197
; GENERAL INFORMATION:
; APPLICANT: Wood, Thomas K.
; APPLICANT: Jayaraman, Arul
; APPLICANT: Earthman, James C.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibition of Sulfate-Reducing-Bacteria-Mediated
; TITLE OF INVENTION: Degradation Using Bacteria Which Secrete Antimicrobials
; FILE REFERENCE: 02307E-085910US
; CURRENT APPLICATION NUMBER: US/09/282,277
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: US 09/074,037
; EARLIER FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:non-amidated
; OTHER INFORMATION: bactenecin
US-09-282-277-9

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
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Db 1 RLCRIWVIRVCR 12

RESULT 5

US-09-917-340-37
; Sequence 37, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:

; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-37

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

RESULT 6
US-09-623-548A-1022
; Sequence 1022, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1022
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-1022

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | | | |
Db 1 RLCRIWVIRVCR 12

RESULT 7
US-09-623-548A-1031
; Sequence 1031, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1031
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-1031

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
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Db 1 RLCRIWVIRVCR 12

RESULT 8
US-09-657-276-1022
; Sequence 1022, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1022
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-1022

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1022

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
| | | | | | | | | |
DB 1 RLCRIVVIRVCR 12

RESULT 9
US-09-657-276-1031
; Sequence 1031, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaut, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1031
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1031

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
| | | | | | | | | |
DB 1 RLCRIVVIRVCR 12

RESULT 10
US-09-444-281-42
; Sequence 42, Application US/09444281
; Patent No. 6946261
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/09/444,281
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 12
; TYPE: PRT

; ORGANISM: Bos taurus
US-09-444-281-42

Query Match 100.0%; Score 62; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
| | | | | | | | | |
DB 1 RLCRIVVIRVCR 12

RESULT 11
US-09-082-420-11
; Sequence 11, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-11

Query Match 100.0%; Score 62; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
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DB 2 RLCRIVVIRVCR 13

RESULT 12
US-09-082-420-18
; Sequence 18, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-18

Query Match 100.0%; Score 62; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVCR 12
| | | | | | | | | |
DB 1 RLCRIVVIRVCR 12

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RESULT 13
US-09-282-277-3
; Sequence 3 Application US/09282277
; Patent No. 6630197
; GENERAL INFORMATION:
; APPLICANT: Wood, Thomas K.
; APPLICANT: Jayaraman, Arul
; APPLICANT: Earhman, James C.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibition of Sulfate-Reducing-Bacteria-Mediated
; TITLE OF INVENTION: Degradation Using Bacteria Which Secrete Antimicrobials
; FILE REFERENCE: 02307E-085910US
; CURRENT APPLICATION NUMBER: US/09/282,277
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: US 09/074,037
; EARLIER FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pro-bactenecin
; OTHER INFORMATION: pro-region and bactenecin
US-09-282-277-3

Query Match 100.0%; Score 62; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 RLCRIWIRVCR 12
DB 14 RLCRIWIRVCR 25

RESULT 14
US-09-917-340-29
; Sequence 29, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-29

Query Match 100.0%; Score 62; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 RLCRIWIRVCR 12
DB 144 RLCRIWIRVCR 155

RESULT 15

```

```
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-13

Query Match      83.1%; Score 51.5; DB 2; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.052;
Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 RLCRIV-VIRVCR 12
Db      1 RLCRIVWVIRVCR 13

RESULT 18
US-09-082-420-14
; Sequence 14, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-14

Query Match      83.1%; Score 51.5; DB 2; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.059;
Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 RLCRIV-VIRVCR 12
Db      2 RLCRIVWVIRVCR 14

RESULT 19
US-09-082-420-5
; Sequence 5, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: cationic antimicrobial peptide
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: amidated Arg at C-terminus
US-09-082-420-5

Query Match      79.0%; Score 49; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVCR 12
Db      1 RRCPIVVIRVCR 12

RESULT 20
US-09-082-420-20
; Sequence 20, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-20

Query Match      79.0%; Score 49; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVCR 12
Db      1 RRCPIVVIRVCR 12

RESULT 21
US-09-082-420-9
; Sequence 9, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-9

Query Match      79.0%; Score 49; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 RLCRIWVIRVCR 12
| | | | | | | |
Db 2 RRCPIWVIRVCR 13

RESULT 22
US-09-904-753-12
; Sequence 12, Application US/09904753
; Patent No. 6872705
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: Use of Antimicrobial Peptides as Preservatives in
; TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions,
; TITLE OF INVENTION: Emulsions, and Suspensions
; FILE REFERENCE: 2973 ver 2
; CURRENT APPLICATION NUMBER: US/09/904,753
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: WO 96/25183
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: COW
US-09-904-753-12

Query Match 76.6%; Score 47.5; DB 2; Length 11;
Best Local Similarity 91.7%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | |
Db 1 RLCR-WVIRVCR 11

RESULT 23
US-09-882-420-6
; Sequence 6, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECCIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: amidated Arg at C-terminus
US-09-882-420-6

Query Match 72.6%; Score 45; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 0.49;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | |
Db 1 RICRIWVIRVCR 12

RESULT 24
US-09-882-420-2

; Sequence 2, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECCIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: amidated Arg at C-terminus
US-09-882-420-2

Query Match 71.0%; Score 44; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | |
Db 1 RLARIWVIRVAR 12

RESULT 25
US-09-030-619-127
; Sequence 127, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 127
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-127

Query Match 71.0%; Score 44; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
| | | | | | | |
Db 1 RLARIWVIRVAR 12

RESULT 26
US-10-225-087-118
; Sequence 118, Application US/10225087
; Patent No. 6835536

```
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: McNicol, Patricia J.
; APPLICANT: Fraser, Janet R.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND
; TITLE OF INVENTION: FORMULATIONS THEREOF
; FILE REFERENCE: 660081.417
; CURRENT APPLICATION NUMBER: US/10/225,087
; CURRENT FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin analog
US-10-225-087-118

Query Match          71.0%; Score 44; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 RLCRIWVIRVC 12
DB      1 RLRIWVIRVAR 12

RESULT 27
US-09-082-420-8
; Sequence 8, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-8

Query Match          69.4%; Score 43; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.99;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 CRIWVIRVC 12
DB      3 CPIWVIRVCK 12

RESULT 28
US-09-082-420-4
; Sequence 4, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
;
```

```
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: amidated Arg at C-terminus
US-09-082-420-4

Query Match          67.7%; Score 42; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 RLCRIWVIRVC 12
DB      1 RLSRIWVIRVSR 12

RESULT 29
US-09-082-420-19
; Sequence 19, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-19

Query Match          67.7%; Score 42; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 RLCRIWVIRVC 12
DB      1 RLSRIWVIRVSR 12

RESULT 30
US-09-082-420-7
; Sequence 7, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
;
```


; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: amidated Arg at C-terminus
US-09-082-420-7

Query Match 66.1%; Score 41; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

Qy 1 RLCRIWVIRVCR 12
Db 1 RLCPRVIRVCR 12

RESULT 31

US-09-082-420-10

; Sequence 10, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
US-09-082-420-10

Query Match 65.3%; Score 40.5; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.8;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 RLCRIWVIRVCR 12
Db 3 RLCPI-VIRVCR 13

RESULT 32

US-09-082-420-15

; Sequence 15, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: amidated Arg at C-terminus
US-09-082-420-15

Query Match 62.1%; Score 38.5; DB 2; Length 13;
Best Local Similarity 76.9%; Pred. No. 5.3;

Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 1 RLCRIWVIRVCR 12
Db 1 RLCPIWVIRVCR 13

RESULT 33

US-09-252-991A-30203
; Sequence 30203, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30203
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30203

Query Match 59.7%; Score 37; DB 2; Length 181;
Best Local Similarity 63.6%; Pred. No. 96;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 12
Db 137 LCRSVVRSR 147

RESULT 34

US-09-270-767-41347
; Sequence 41347, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41347
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41347

Query Match 58.1%; Score 36; DB 2; Length 152;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVIRVCR 11
Db 106 LCECVXRVRC 115

RESULT 35

US-09-270-767-56563
; Sequence 56563, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.

```

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56563
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-65663

Query Match      58.1%; Score 36; DB 2; Length 152;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 LCRIVRVRC 11
Db      106 LCECVXVRVC 115

RESULT 36
US-09-270-767-45575
; Sequence 45575, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45575
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45575

Query Match      58.1%; Score 36; DB 2; Length 318;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CRIVRVRCR 12
Db      202 CRVLSRXCR 211

RESULT 37
US-09-107-532A-4947
; Sequence 4947, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII

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```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4947:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...334
; SEQUENCE DESCRIPTION: SEQ ID NO: 4947:
US-09-107-532A-4947

Query Match      58.1%; Score 36; DB 2; Length 334;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RLCRIVVIRVC 12
Db      1 RLCKIIRKVC 12

RESULT 38
US-08-911-423-6
; Sequence 6, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:

```

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-423-6

Query Match 56.5%; Score 35; DB 2; Length 228;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RLCRIWVIRVCR 12
DB 42 RCCRVTTRCCR 53

RESULT 39

US-08-911-423-7
Sequence 7, Application US/08911423
Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-423-7

Query Match 56.5%; Score 35; DB 2; Length 232;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RLCRIWVIRVCR 12
DB 42 RCCRVTTRCCR 53

RESULT 40

US-09-512-363-2
Sequence 2, Application US/09512363
Patent No. 6503184
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Tril1, Trl1SV1, and Trl1SV2
FILE REFERENCE: PF396
CURRENT APPLICATION NUMBER: US/09/512,363
CURRENT FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: 60/063,212
EARLIER FILING DATE: 1997-10-21
EARLIER APPLICATION NUMBER: 09/176,200
EARLIER FILING DATE: 1998-10-21
EARLIER APPLICATION NUMBER: 60/121,648
EARLIER FILING DATE: 1999-02-24
EARLIER APPLICATION NUMBER: 60/134,172
EARLIER FILING DATE: 1999-05-13
EARLIER APPLICATION NUMBER: 60/144,076
EARLIER FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
US-09-512-363-2

Query Match 56.5%; Score 35; DB 2; Length 234;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RLCRIWVIRVCR 12
DB 48 RCCRVTTRCCR 59

RESULT 41

US-09-176-200-2
Sequence 2, Application US/09176200
Patent No. 6509173
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Trl1, Trl1SV1, and Trl1SV2
FILE REFERENCE: PF396
CURRENT APPLICATION NUMBER: US/09/176,200
CURRENT FILING DATE: 1998-10-21
EARLIER APPLICATION NUMBER: 60/063,212
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
US-09-176-200-2

Query Match 56.5%; Score 35; DB 2; Length 234;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-512-363-6

Query Match      56.5%; Score 35; DB 2; Length 240;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches        6; Conservative    1; Mismatches    5; Indels    0; Gaps    0;

Qy      1 RLCRIVIRVCR 12
Db      42 RCCRVTTRCCR 53

RESULT 44
US-09-176-200-6
; Sequence 6, Application US/09176200
; Patent No. 6509173
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/176,200
; CURRENT FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-176-200-6

Query Match      56.5%; Score 35; DB 2; Length 240;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches        6; Conservative    1; Mismatches    5; Indels    0; Gaps    0;

Qy      1 RLCRIVIRVCR 12
Db      42 RCCRVTTRCCR 53

RESULT 45
US-09-915-593-6
; Sequence 6, Application US/09915593
; Patent No. 6689607
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-593-6

Query Match 56.5%; Score 35; DB 2; Length 240;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RLCRVIVRVC 12
Db 42 RCRVHTTRCC 53

RESULT 46
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4

Query Match 56.5%; Score 35; DB 2; Length 241;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RLCRVIVRVC 12
Db 48 RCRVHTTRCC 59

RESULT 47
US-09-512-363-28
; Sequence 28, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/512,363
; CURRENT FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; EARLIER APPLICATION NUMBER: 09/176,200
; EARLIER FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/121,648
; EARLIER FILING DATE: 1999-02-24
; EARLIER APPLICATION NUMBER: 60/134,172
; EARLIER FILING DATE: 1999-05-13
; EARLIER APPLICATION NUMBER: 60/144,076
; EARLIER FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-512-363-28

Query Match 56.5%; Score 35; DB 2; Length 241;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RLCRVIVRVC 12
Db 48 RCRVHTTRCC 59

RESULT 48
US-09-915-593-28
; Sequence 28, Application US/09915593
; Patent No. 6689607
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-593-28

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Query Match          56.5%; Score 35; DB 2; Length 241;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
   |||: |||
Db 48 RCRVHTTCRCR 59

RESULT 49
US-09-949-016-7232
; Sequence 7232, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7232
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7232

Query Match          56.5%; Score 35; DB 2; Length 241;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
   |||: |||
Db 48 RCRVHTTCRCR 59

RESULT 50
US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-911-423-8

Query Match          56.5%; Score 35; DB 2; Length 311;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
   |||: |||
Db 42 RCRVHTTCRCR 53

RESULT 51
US-09-134-000C-6570
; Sequence 6570, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6570
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-6570

Query Match          54.8%; Score 34; DB 2; Length 116;
Best Local Similarity 45.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 11
   :||| |||: |||
Db 8 KVCIVVCLKVC 18

RESULT 52
US-09-583-110-3039
; Sequence 3039, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
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; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3039
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3039

Query Match 54.8%; Score 34; DB 2; Length 209;
Best Local Similarity 36.4%; Pred. No. 3.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LRCRIVWVRC 11
| | | : : :
Db 7 RSCRLTKVKIC 17

RESULT 53

US-09-107-433-4632
; Sequence 4632, Application US/09107433
; Patent No. 6800744

GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/POCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4632:

SEQUENCE CHARACTERISTICS:

; LENGTH: 217 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...217
; SEQUENCE DESCRIPTION: SEQ ID NO: 4632:
US-09-107-433-4632

Query Match 54.8%; Score 34; DB 2; Length 217;
Best Local Similarity 36.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LRCRIVWVRC 11
| | | : : :
Db 15 RSCRLTKVKIC 25

RESULT 54

US-09-248-796A-19531
; Sequence 19531, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 19531

; LENGTH: 971

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-19531

Query Match 54.8%; Score 34; DB 2; Length 971;
Best Local Similarity 45.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVWVRC 12
| | | : : :
Db 841 LCDIMVFMCK 851

RESULT 55

US-09-270-767-60996
; Sequence 60996, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 60996

; LENGTH: 38

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-60996

Query Match 53.2%; Score 33; DB 2; Length 38;
Best Local Similarity 36.4%; Pred. No. 98;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVWVRC 12
| | | : : :
Db 24 MCLLEVLQICR 34

RESULT 56

US-09-270-767-35000
; Sequence 35000, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35000
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-35000

Query Match 53.2%; Score 33; DB 2; Length 69;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LCRIVVIRVC 11
:|:|:|
Db 32 ICRILACRYC 41

RESULT 57
US-09-270-767-50217
; Sequence 50217, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50217
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-50217

Query Match 53.2%; Score 33; DB 2; Length 69;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LCRIVVIRVC 11
:|:|:|
Db 32 ICRILACRYC 41

RESULT 58
US-09-134-000C-5671
; Sequence 5671, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5671
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5671

Query Match 53.2%; Score 33; DB 2; Length 114;
Best Local Similarity 41.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LCRIVVIRVC 12

Db 28 QLCRVVTVKGAR 39
:|:|:|:|:|

RESULT 59
US-09-270-767-37838
; Sequence 37838, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37838
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-37838

Query Match 53.2%; Score 33; DB 2; Length 120;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVC 12
:|:|:|:|:|
Db 68 RLCVCCVLTVCCK 79

RESULT 60
US-09-270-767-53055
; Sequence 53055, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53055
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53055

Query Match 53.2%; Score 33; DB 2; Length 120;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RLCRIVVIRVC 12
:|:|:|:|:|
Db 68 RLCVCCVLTVCCK 79

RESULT 61
US-09-270-767-45487
; Sequence 45487, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45487
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45487

Query Match 53.2%; Score 33; DB 2; Length 166;
Best Local Similarity 36.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVVIRVCR 12
| : : : : :
Db 152 MCLLEVQLQICR 162

RESULT 62

US-09-252-991A-26289
; Sequence 26289, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26289
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26289

Query Match 53.2%; Score 33; DB 2; Length 231;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LCRIVWI 8
| : : : : :
Db 38 RLCRICV 45

RESULT 63

US-09-902-540-10473
; Sequence 10473, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10473
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10473

Query Match 53.2%; Score 33; DB 2; Length 264;
Best Local Similarity 58.3%; Pred. No. 5.6e+02;

Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 RLCRIWIRVCR 12
| : : : : :
Db 200 RYCRTIVIEPAR 211

RESULT 64

US-09-198-452A-1201
; Sequence 1201, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; FILE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1201
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1201

Query Match 53.2%; Score 33; DB 2; Length 279;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVWIRVC 11
| : : : : :
Db 43 LCALLIILVC 52

RESULT 65

US-09-438-185A-519
; Sequence 519, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 519
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CFP0517
US-09-438-185A-519

Query Match 53.2%; Score 33; DB 2; Length 281;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LCRIVWIRVC 11
| : : : : :
Db 45 LCALLIILVC 54

RESULT 66

```
US-10-104-047-3458
; Sequence 3458, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3458
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3458

Query Match      53.2%; Score 33; DB 2; Length 315;
Best Local Similarity 45.5%; Pred. No. 6.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RLCRIWVIRVC 11
Db      106 RLCYLVAETIC 116

RESULT 67
US-09-809-665A-115
; Sequence 115, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-809-665A-115

Query Match      53.2%; Score 33; DB 2; Length 396;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 CRIWVIRV 10
Db      80 CKVIVRV 87

RESULT 68
US-09-809-665A-50
; Sequence 50, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-809-665A-50

Query Match      53.2%; Score 33; DB 2; Length 398;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 CRIWVIRV 10
Db      82 CKVIVRV 89

RESULT 69
US-07-969-267B-3
; Sequence 3, Application US/07969267B
; Patent No. 5882855
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Hartig, Paul R.
; TITLE OF INVENTION: DNA Encoding A Human Dopamine D1
; TITLE OF INVENTION: Receptor And Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,267B
; FILING DATE: 05-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/551,448
; FILING DATE: 10-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-969-267B-3

Query Match      53.2%; Score 33; DB 1; Length 477;
Best Local Similarity 41.7%; Pred. No. 9.6e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 RLCRIWVIRVC 12
Db      248 RYRIAQVQICR 259
```

RESULT 70
US-09-168-510-3
; Sequence 3, Application US/09168510
; Patent No. 6468767
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA Encoding A Human Dopamine D1
; TITLE OF INVENTION: Receptor And Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/168,510
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,267
; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: 07/551,448
; FILING DATE: 10-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-168-510-3
Query Match 53.2%; Score 33; DB 2; Length 477;
Best Local Similarity 41.7%; Pred. No. 9.6e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RLCHRVIRVCR 12
|: || ::||
Db 248 RYRIAQVQICR 259
RESULT 71
US-10-277-078-3
; Sequence 3, Application US/10277078
; Patent No. 6939680
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA Encoding A Human Dopamine D1
; TITLE OF INVENTION: Receptor And Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York

COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/277,078
FILING DATE: 21-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/168,510
FILING DATE: <Unknown>
APPLICATION NUMBER: 07/969,267
FILING DATE: 05-OCT-1993
APPLICATION NUMBER: 07/551,448
FILING DATE: 10-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-277-078-3
Query Match 53.2%; Score 33; DB 2; Length 477;
Best Local Similarity 41.7%; Pred. No. 9.6e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RLCHRVIRVCR 12
|: || ::||
Db 248 RYRIAQVQICR 259
RESULT 72
US-09-949-016-6846
; Sequence 6846, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6846
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(609)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-949-016-6846

```
Query Match          53.2%; Score 33; DB 2; Length 609;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      3 CRIVWVRC 11
      |::|::|
Db      326 CKWVLSVC 334

RESULT 73
US-09-230-371A-30
; Sequence 30, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230.371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human
US-09-230-371A-30

Query Match          52.4%; Score 32.5; DB 2; Length 425;
Best Local Similarity 41.2%; Pred. No. 1e+03;
Matches 7; Conservative 4; Mismatches 1; Indels 5; Gaps 1;

QY      1 RLCR-----IVWVRCR 12
      |||::|::|
Db      290 RLCQGRVFCVVVVVCK 306

RESULT 74
US-09-270-767-44123
; Sequence 44123, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44123
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44123

Query Match          52.4%; Score 32.5; DB 2; Length 631;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
Matches 6; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY      1 RLCRIVVIR-VCR 12
      |||::|::|
Db      141 RICKVSGTRICR 153

RESULT 75
US-09-198-452A-1019
; Sequence 1019, Application US/09198452A
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```
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198.452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1019
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1019

Query Match          51.6%; Score 32; DB 2; Length 97;
Best Local Similarity 25.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY      1 RLCRIVVIRVCR 12
      :|::|::|
Db      7 KTCSLILLNLCR 18

RESULT 76
US-09-732-210-389
; Sequence 389, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732.210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 389
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pinus thunbergii
US-09-732-210-389

Query Match          51.6%; Score 32; DB 2; Length 122;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 RIVVIRVCR 12
      |||||
Db      59 RAVVIRTCR 67

RESULT 77
US-09-902-540-16503
; Sequence 16503, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902.540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
```

```
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16503
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16503

Query Match      51.6%; Score 32; DB 2; Length 126;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VVIVRCR 12
      :::|||
Db      57 IIVRCR 63

RESULT 78
US-09-270-767-35046
; Sequence 35046, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35046
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35046

Query Match      51.6%; Score 32; DB 2; Length 186;
Best Local Similarity 45.5%; Pred. No. 5.9e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RLCRIVRVC 11
      :||: : ||
Db      106 QLCRNIYRVC 116

RESULT 79
US-09-270-767-50263
; Sequence 50263, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50263
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50263

Query Match      51.6%; Score 32; DB 2; Length 186;
Best Local Similarity 45.5%; Pred. No. 5.9e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 RLCRIVRVC 11
      :||: : ||
Db      106 QLCRNIYRVC 116

RESULT 80
US-09-605-703B-2376
; Sequence 2376, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kröger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 2376
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-2376

Query Match      51.6%; Score 32; DB 2; Length 193;
Best Local Similarity 62.5%; Pred. No. 6.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LCRIVVIR 9
      ||: ||: ||
Db      46 LCQIIVLR 53

RESULT 81
US-09-270-767-56833
; Sequence 56833, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56833
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56833

Query Match      51.6%; Score 32; DB 2; Length 216;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RLCRIVVI 8
      ||| ||| ||
Db      79 RLCSIVII 86

RESULT 82
US-09-270-767-33011
; Sequence 33011, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
```

; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33011
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33011

Query Match 51.6%; Score 32; DB 2; Length 257;
Best Local Similarity 58.3%; Pred. No. 7.8e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
| | | | |
Db 219 RACKPVVDVVCR 230

RESULT 83
US-09-270-767-48228
; Sequence 48228, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48228
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48228

Query Match 51.6%; Score 32; DB 2; Length 257;
Best Local Similarity 58.3%; Pred. No. 7.8e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
| | | | |
Db 219 RACKPVVDVVCR 230

RESULT 84
US-09-270-767-35184
; Sequence 35184, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35184
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35184

Query Match 51.6%; Score 32; DB 2; Length 267;
Best Local Similarity 55.6%; Pred. No. 8.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
| | | | |

Db 229 CRSVVIQIC 237

RESULT 85
US-09-270-767-50401
; Sequence 50401, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50401
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50401

Query Match 51.6%; Score 32; DB 2; Length 267;
Best Local Similarity 55.6%; Pred. No. 8.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVVIRVC 11
| | | | |
Db 229 CRSVVIQIC 237

RESULT 86
US-09-540-236-2293
; Sequence 2293, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2293
; LENGTH: 308
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2293

Query Match 51.6%; Score 32; DB 2; Length 308;
Best Local Similarity 41.7%; Pred. No. 9.2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVVIRVCR 12
| | | | |
Db 9 KLCRINILANCQ 20

RESULT 87
US-09-252-991A-26909
; Sequence 26909, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 26909
;; LENGTH: 401
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26909

Query Match 51.6%; Score 32; DB 2; Length 401;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IIVIRVCR 12
|:|:|:|
Db 54 IIVLRLCR 61

RESULT 88
US-09-252-991A-20793
; Sequence 20793, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20793
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20793

Query Match 51.6%; Score 32; DB 2; Length 548;
Best Local Similarity 63.6%; Pred. No. 1.5e+03;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLCRIVIRVC 11
|:|:|:|
Db 489 RLSRVVVEGVC 499

RESULT 89
US-09-437-568A-12
; Sequence 12, Application US/09437568A
; Patent No. 6620603
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
; FILE REFERENCE: 05501-0103
; CURRENT APPLICATION NUMBER: US/09/437,568A
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-437-568A-12

Query Match 51.6%; Score 32; DB 2; Length 569;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
|:|:|:|
Db 63 CMLILLPVC 72

RESULT 90
US-09-999-248A-13
; Sequence 13, Application US/09999248A
; Patent No. 6846872
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Mitogenic Oxygenase Regulators
; FILE REFERENCE: 05501-0180 43150-266489
; CURRENT APPLICATION NUMBER: US/09/999,248A
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/249,305
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/251,364
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/289,172
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/289,537
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-999-248A-13

Query Match 51.6%; Score 32; DB 2; Length 569;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
|:|:|:|
Db 63 CMLILLPVC 72

RESULT 91
US-09-437-568A-37
; Sequence 37, Application US/09437568A
; Patent No. 6620603
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
; FILE REFERENCE: 05501-0103
; CURRENT APPLICATION NUMBER: US/09/437,568A
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Bovine
US-09-437-568A-37

Query Match 51.6%; Score 32; DB 2; Length 570;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIVRVC 12
|:|:|:|
Db 64 CMLILLPVC 73

```
RESULT 92
US-09-437-568A-38
; Sequence 38, Application US/09437568A
; Patent No. 6620603
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
; CURRENT APPLICATION NUMBER: US/09/437,568A
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 570
; TYPE: PRT
; ORGANISM: murine
US-09-437-568A-38

Query Match 51.6%; Score 32; DB 2; Length 570;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIRVCR 12
| : : : |
Db 64 CMLILLPVCR 73

RESULT 93
US-10-418-036-2
; Sequence 2, Application US/10418036
; Patent No. 6893833
; GENERAL INFORMATION:
; APPLICANT: Gronberg, Alvar
; APPLICANT: Wikstrom, Per
; TITLE OF INVENTION: NEW USE
; FILE REFERENCE: I3425-110001
; CURRENT APPLICATION NUMBER: US/10/418,036
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: SE 0201152-6
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/410,626
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-036-2

Query Match 51.6%; Score 32; DB 2; Length 570;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CRIVIRVCR 12
| : : : |
Db 64 CMLILLPVCR 73

RESULT 94
US-09-252-991A-25700
; Sequence 25700, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
```

```
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25700
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25700

Query Match 51.6%; Score 32; DB 2; Length 710;
Best Local Similarity 45.5%; Pred. No. 2e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVCR 12
| : : : |
Db 217 LCRVCLHKPCR 227

RESULT 95
US-09-693-146-4
; Sequence 4, Application US/09693146
; Patent No. 6413758
; GENERAL INFORMATION:
; APPLICANT: Xu, Shuang-yong
; APPLICANT: Zhu, Zhenyu
; APPLICANT: Xiao, Jian-ping
; TITLE OF INVENTION: Method For Cloning And Expression Of Bpm1 Restriction
; TITLE OF INVENTION: Endonuclease In E. coli
; FILE REFERENCE: NEB-183
; CURRENT APPLICATION NUMBER: US/09/693,146
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1009
; TYPE: PRT
; ORGANISM: Bacillus pumilus
US-09-693-146-4

Query Match 51.6%; Score 32; DB 2; Length 1009;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LCRIVVIRVCR 11
| : : : |
Db 228 LNRILFLRVC 237

RESULT 96
US-09-082-420-16
; Sequence 16, Application US/09082420
; Patent No. 6172185
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Wu, Manhong
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDE
; TITLE OF INVENTION: DERIVATIVES OF BACTENECIN
; FILE REFERENCE: 07422/017001
; CURRENT APPLICATION NUMBER: US/09/082,420
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cationic antimicrobial peptide
; FEATURE:
; NAME/KEY: AMIDATION
```


; LOCATION: (O)...(O)
; OTHER INFORMATION: amidated Arg at C-terminus
US-09-082-420-16

Query Match 50.8%; Score 31.5; DB 2; Length 14;
Best Local Similarity 69.2%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 RLCRIV-VIRVCR 12
|:|:|:|:|:|
Db 1 RRCPIVWIPVCR 13

RESULT 97
US-09-513-999C-4573
; Sequence 4573, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4573
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46...-1
; OTHER INFORMATION: score 6.5
; OTHER INFORMATION: seq WLFPLMLSLCTPP/DR
US-09-513-999C-4573

Query Match 50.8%; Score 31.5; DB 2; Length 56;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 RLCRIV-VIRVC 11
|:|:|:|:|:|
Db 3 RMCRFVTWIVNC 14

RESULT 98
US-09-471-276-1013
; Sequence 1013, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1013
; LENGTH: 57

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46...-1
US-09-471-276-1013

Query Match 50.8%; Score 31.5; DB 2; Length 57;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 RLCRIV-VIRVC 11
|:|:|:|:|:|
Db 3 RMCRFVTWIVNC 14

RESULT 99
US-08-685-589A-141
; Sequence 141, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..16
; OTHER INFORMATION: /product= "Cyclic"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /product= "Xaa=D-Arginine"
US-08-685-589A-141

Query Match 50.0%; Score 31; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 92;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RLCRIWVIRVC 11
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Db 3 RYCRXFCVRF 13

RESULT 100

US-09-621-976-5254
; Sequence 5254, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5254
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
US-09-621-976-5254

Query Match 50.0%; Score 31; DB 2; Length 52;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LCRIVWIRVC 11
: | | : | |
Db 18 VCACVSVRVC 27

Search completed: February 15, 2006, 11:11:49
Job time : 48 secs